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(57) Abstract: Disclosed are artificial chromosomes based on centromeric sequences having specific alphoid repeats and alpha
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APPLICATION

TITLE

**ARTIFICIAL CHROMOSOMES THAT CAN SHUTTLE
BETWEEN BACTERIA, YEAST, AND MAMMALIAN CELLS**

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I. CROSS REFERENCE TO RELATED APPLICATION

This application claims priority to U.S. application Serial No. 60/282,010, filed April 6, 2001, which is hereby incorporated in its entirety.

II. STATEMENT OF GOVERNMENT RIGHTS

15 This invention was made with government support provided National Institutes of Health The government has certain rights in the invention.

III. BACKGROUND OF THE INVENTION

Successful development of a Human Artificial Chromosome (HAC) cloning system would have profound effects on human gene therapy and on our understanding of the organization of human centromeric regions and a kinetochore function. Efforts so far to produce HACs have involved two basic approaches: paring down an existing functional chromosome, or building upward from DNA sequences that could potentially serve as functional elements. The first approach utilized telomere-directed chromosome fragmentation to systematically decrease chromosome size, while maintaining correct chromosomal function. The fragmentation has been targeted to both the X and Y chromosome centromere sequences by incorporating homologous

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25

5 sequences into the fragmentation vector. This approach has pared the Y and X
chromosomes down to a minimal size of ~2.0 Mb which can be stably maintain in
culture (Heller et al., *Proc. Natl. Acad. Sci. USA* 93:7125-7130, 1996; Mills et al. *Hum.*
Mol. Genet. 8: 751-761, 1999; Kuroiwa et al., *Nature Biotech.* 18: 1086-1090, 2000).
These deleted chromosome derivatives lost most of their chromosomal arms and up to
10 90% of their alphoid DNA array. None of the mitotically stable derivatives contained
alphoid DNA arrays shorter than ~100 kb, suggesting that this size block of alphoid
DNA alone or along with the short arm flanking sequence is sufficient for a centromere
function.

The second approach was based on transfection of human cells by YAC or BAC
15 constructs containing large arrays of alphoid DNA (Harrington et al., *Nat. Genet.* 15:
345-355, 1997; Ikeno et al., *Nature Biotech.* 16: 431-439, 1998; Henning et al., *Proc.*
Nat. Acad. Sci. 96: 592-597, 1999; Ebersole et al., *Hum. Mol. Genet.* 9:1623-1631,
2000). Because the formation of HACs was not observed with constructs containing
random genomic fragments, these experiments clearly demonstrated an absolute
20 requirement of alphoid DNA for centromere function. In all cases formation of HACs
was accompanied by 10-50-fold amplification of YAC/BAC constructs in transfected
cells.

Both approaches led to development of cell lines containing genetically marked
chromosomal fragments exhibiting a stable maintenance during cell divisions. These
25 mini-chromosomes appear to be linear and about 2-12 Mb in size. An obvious
limitation of the systems described above is the large size of HACs that prohibits their
cloning and manipulation in microorganisms, rendering transfer to other mammalian
cell types difficult. Disclosed herein are methods and compositions which allow for the
specific cloning of centromeric regions from mammalian chromosomes. Disclosed are
30 cloned and isolated centromeric regions of human and other mammalian chromosomes.
The isolation of these centromeric regions provides for mammalian artificial
chromosomes (MACs) capable of being shuttled between bacterial, yeast and

5 mammalian cells, such as human cells. The isolation of a functional centromere from centromeric regions of human chromosomes, including the mini-chromosome $\Delta Yq74$ containing 12 Mb of the Y human chromosome (Heller et al., Proc. Natl. Acad. Sci. Usa 93:7125-7130,1996), and the human chromosome 22, is disclosed. The centromeric regions were isolated from total genomic DNA by using a novel protocol
10 of Transformation-Associated Recombination (TAR) in yeast technique which is disclosed herein. TAR is a cloning technique based on in vivo recombination in yeast (Larionov et al., Proc. Natl. Acad. Sci. USA 93:13925-13930,1996; Kouprina et al., Proc. Natl. Acad. Sci. USA 95: 4469-4474,1998; Kouprina and Larionov Current protocols in Human genetics 5.17.1-5.17.21,1999). These MACs provide useful
15 vehicles for the delivery and expression of transgenes within cells and as tools for the isolation and characterization of genes and other DNA sequences.

IV. SUMMARY OF THE INVENTION

In accordance with the purposes of this invention, as embodied and broadly described herein, this invention, in one aspect, relates to a mammalian artificial
20 chromosome which in one embodiment can be represented by the structure Y-X-Z-Y.

These mammalian chromosomes function much like natural chromosomes in that they replicate and segregate appropriately during the cell cycle. As discussed below these MACs can contain DNA that is expressed within a cell. The MACs can also be configured with sequences that allow them to function as bacterial artificial
25 chromosomes (BACs) as well as sequences that allow them to function as yeast artificial chromosomes (YACs). Thus, specialized shuttle vectors, which allow the artificial chromosomes to be replicated and segregated in either mammalian cells, such as human cells, bacterial cells, and yeast cells are disclosed.

The mammalian artificial chromosome can act as a shuttle vector which can be
30 shuttled between BACs, YACs, and MACs, in any or all combinations.

5 Additional advantages of the invention will be set forth in part in the description which follows, and in part will be obvious from the description, or may be learned by practice of the invention. The advantages of the invention will be realized and attained by means of the elements and combinations particularly pointed out in the appended claims. It is to be understood that both the foregoing general description and the
10 following detailed description are exemplary and explanatory only and are not restrictive of the invention, as claimed.

V. BRIEF DESCRIPTION OF THE DRAWINGS

The accompanying drawings, which are incorporated in and constitute a part of this specification, illustrate several embodiments of the invention and together with the
15 description, serve to explain the principles of the invention.

Figure 1 shows a schematic of a selective isolation of a centromeric region by a TAR vector with a counter-selectable marker. An ARS element is included into a TAR vector containing the HIS3 selectable marker, CEN as a yeast centromeric region, and two targeting sequences (Sat). To avoid a high background resulting from re-
20 circularization of an ARS-containing vector during yeast transformation (Noskov et al., Nucleic Acids. Res., 29(6):e32 (2001) a counter-selectable marker, SUP11, was included between specific targeting sequences in the vector. SUP11 encodes an ochre suppresser tRNA and as it was shown by, even one copy of the gene is highly toxic for a prion-containing (psi-plus) yeast strain. As a consequencce, autonomously replicating
25 plasmids carrying SUP11 transform yeast cells very poorly. In addition, SUP11 suppresses an ade2-101 mutation in a host strain. Ade2-101 cells are red while in the presence of SUP11 they are white. Homologous recombination between the targeting sequences and human centromeric DNA would result in generation of a circular YAC accompanied by a loss of the SUP11 sequence. Colonies with such YACs should be
30 red. These two phenotypes caused by a loss of SUP11 provide a selectivity of isolation of human centromeric regions.

5 Figure 2 shows a schematic of the macrostructure repeating unit that makes up the centromere region isolated from human chromosome Y.

 Figure 3 shows a sequence comparison of the 34 alpha satellites that make up a part of the repeating unit of the chromosome Y centomeric DNA. The homologies and identity of these sequences are disclosed within this figure, by looking at the variation
10 between the various sequences. See SEQ ID NOs: 4-37.

 Figure 4 shows the sequence of the 1.6 kb minor Spe I fragment of the $\Delta Yq74$ alphoid DNA region. The junction between tandem and inverted repeats is shown by underlined letters. The sequence is read 5' to 3'. See SEQ ID NO:1.

 Figure 5A shows a phylogenetic tree for 30 sequences of the about 170 base
15 alpha satellite sequences that make up the main Spe I fragments of the $\Delta Yq74$ alphoid region of the Y chromosome. Figure 5B shows a phylogenetic tree for 30 sequences of the about 170 base alpha satellite sequences that make up the main alphoid region of chromosome 22.

 Figure 6 shows the sequence of the pVC-sat vector used for TAR cloning of
20 centromeric regions and alphoid repeat DNA. The sequence is read 5' to 3'. See SEQ ID NO: 51.

 Figure 7 shows the sequence of the 2.9 kb major fragment of the SpeI digestion of the chromosome Y alphoid region. The sequence is read 5' to 3'. See SEQ ID
NO:3.

25 Figure 8 shows the sequence of the 2.8 kb major fragment of the SpeI digestion of the chromosome Y alphoid region. The sequence is read 5' to 3'. See SEQ ID NO:2.

5 Figure 9A shows comparison of alphoid DNA units from alphoid DNA array isolated from the Y chromosome. These repeat units were selected from the beginning of five 2.9 kb alphoid DNA unit (SpeI fragment). The sequences are read 5' to 3'.

 Figure 9B shows a comparison of 4 inverted repeat units from the 1.6 kb alphoid DNA unit of the Y chromosome.

10 Figure 10 shows how a 2.8 kb Y chromosome alphoid DNA unit was sequenced. There are a lot of base changes in the repeats resulting in a loss or generation of new restriction sites. This polymorphism helped to read through all repeats in the units.

 Figure 11 shows how a 2.9 kb Y chromosome alphoid DNA unit was
15 sequenced. There are a lot of base changes in the repeats resulting in a loss or generation of new restriction sites. This polymorphism helped to read through all repeats in the units.

 Figure 12 shows the orientation of the 34 alpha satellites that make up the 5.7 kb I EcoRI fragment of the chromosome Y alphoid region. Comparison of these units
20 are shown in figure 3.

 Fig. 13 shows two color FISH of BACs (Spectrum Orange) and (Spectrum Geen) to normal human metaphase hybridization of both probes to centromere of chromosome 22. Fiber FISH using the same probes (bottom) demonstrates and overlap of BACs and presence of two separate tandem blocks. Figure 14 shows a gel indicating
25 that alphoid DNA arrays isolated from chromosome 22 consist of two main units, 2.1 kb and 2.8 kb.

 Figure 15 shows a FISH mapping of TAR isolates from the human chromosome
15.

5 Figure 16 shows a schematic of the principal of TAR cloning.

 Figure 17 shows a scheme of retrofitting vectors containing different mammalian selectable markers.

 Figure 18 shows a schematic of the macrostructure repeating unit that makes up the centromere region isolated from chromosome 13.

10 Figure 19 shows a schematic of the macrostructure repeating unit that makes up the centromere region isolated from chromosome 22.

 Figure 20 shows different TAR isolates of alphoid DNA arrays from chromosome 22. EcoRI digestion of BAC DNAs identifies the presence of regular and unregular blocks of alphoid DNA in the centromeric region of this chromosome.

15 Figure 21A and 21B show FISH analysis of metaphase chromosome spreads of HAC cell line generated with the chromosome 22 alphoid HAC construct. Position of HAC (shown by arrow) was detected loose on co-localization of the 22 alphoid DNA probe and vector probe (i.e., BAC vector used for cloning of alphoid DNA array), which colocalize at minichromosome (shown by arrow).

20 Figure 22 shows a digestion of the BACs by SpeI that produced two fragments with size 2.8 kb and 2.9 kb.

 Figure 23 shows the position of the Autonomously Replicating Sequence (ARS) within the alphoid DNA array isolated from human chromosome 22. This alphoid DNA array can form artificial chromosomes in human cells (as shown in Fig. 21). The
25 ARS consensus that is required to initiate DNA replication in yeast is shown on the top.

VI. DETAILED DESCRIPTION

The present invention may be understood more readily by reference to the following detailed description of preferred embodiments of the invention and the

- 5 Examples included therein and to the Figures and their previous and following description.

Before the present compounds, compositions, articles, devices, and/or methods are disclosed and described, it is to be understood that this invention is not limited to specific synthetic methods, specific recombinant biotechnology methods unless
10 otherwise specified, or to particular reagents unless otherwise specified, as such may, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only and is not intended to be limiting.

As used in the specification and the appended claims, the singular forms "a," "an" and "the" include plural referents unless the context clearly dictates otherwise.
15 Thus, for example, reference to "a pharmaceutical carrier" includes mixtures of two or more such carriers, and the like.

Ranges may be expressed herein as from "about" one particular value, and/or to "about" another particular value. When such a range is expressed, another embodiment includes from the one particular value and/or to the other particular value. Similarly,
20 when values are expressed as approximations, by use of the antecedent "about," it will be understood that the particular value forms another embodiment. It will be further understood that the endpoints of each of the ranges are significant both in relation to the other endpoint, and independently of the other endpoint.

In this specification and in the claims which follow, reference will be made to a
25 number of terms which shall be defined to have the following meanings:

"Optional" or "optionally" means that the subsequently described event or circumstance may or may not occur, and that the description includes instances where said event or circumstance occurs and instances where it does not.

Reference will now be made in detail to the present preferred embodiments of
30 the invention, an examples of which is are illustrated in the accompanying drawings.

- 5 Wherever possible, the same reference numbers are used throughout the drawings to refer to the same or like parts.

A. Compositions

- Disclosed are mammalian artificial chromosomes comprising the structure Y-X-Z-Y, wherein the mammalian artificial chromosome can be shuttled between bacteria,
10 yeast, or mammalian cells without alteration of the mammalian chromosome. Also disclosed are mammalian artificial chromosomes comprising the structure Y-X-Z-Y, wherein Z comprises a sequence less than about 250 kb and which is capable of correctly segregating the mammalian artificial chromosome. Also disclosed are mammalian artificial chromosomes wherein Z further comprises a sequence less than
15 about 150 kb. Mammalian artificial chromosome of wherein Z further comprises a sequence less than about 100 kb are also disclosed.

Disclosed are mammalian artificial chromosomes wherein Z comprises an inverted repeat sequence having at least 80% identity to SEQ ID NO:1.

- Disclosed are mammalian artificial chromosomes wherein Z comprises a
20 nucleic acid sequence that lacks a functional CENP-B box sequence.

Disclosed are mammalian artificial chromosomes, wherein Z further alphoid DNA. Also disclosed are mammalian artificial chromosomes, wherein the alphoid DNA is derived from the chromosome 22 centromere and the Y-chromosome centromere.

- 25 Disclosed are mammalian artificial chromosomes, wherein the alphoid DNA consists of 12, 16, 23, 28 or 34 alpha satellite repeats.

Disclosed are mammalian artificial chromosomes comprising the structure Y-X-Z-Y, wherein Z comprises an inverted repeat sequence.

5 Disclosed are mammalian artificial chromosomes comprising the structure Y-X-Z-Y, wherein Z comprises a nucleic acid sequence that lacks a functional CENP-B box sequence.

 Disclosed are shuttle vectors comprising the disclosed mammalian artificial chromosomes which can be shuttled between BACs, YACs, and MACs, in any or all
10 combinations.

 Also disclosed are methods for isolating repeat sequence comprising using a TAR cloning method further comprising a selectable marker for non-insert recombinants and sequence capable of hybridizing to the target repeat sequence.

 Also disclosed are cloning vectors comprising alphoid specific DNA hooks and
15 a marker which indicates whether the vector has recombined with the target sequence or has recombined with itself.

 Disclosed are mammalian artificial chromosomes (MAC). These mammalian chromosomes function much like natural chromosomes in that they replicate and segregate appropriately during the cell cycle. As discussed below these MACs can
20 contain DNA that is expressed within a cell. The MACs can also be configured with sequences that allow them to function as bacterial artificial chromosomes (BACs) as well as sequences that allow them to function as yeast artificial chromosomes (YACs). Thus, specialized shuttle vectors, which allow the artificial chromosomes to be replicated and segregated in either mammalian cells, such as human cells, bacterial
25 cells, and yeast cells are disclosed.

1. Mammalian artificial chromosomes

 The disclosed MACs consist of a number of different parts and can range in size. The disclosed MACs also have a number of properties and characteristics which can be used to describe them. MACs would include for example, artificial

- 5 chromosomes capable of being used in humans, monkeys, apes, chimpanzees, bovines, ovines, ungulates, murines, mice, and rat.

a) Size

The size of the MACs is dictated by, for example, the size of the parts that are required for the MAC to function as a MAC and the size of the parts which are make up
10 the MAC, but which are not required for the MAC to function as a MAC. The size is also dictated by how the MACs are going to be used, for example whether they will be shuttled between bacterial and/or yeast cells. Typically the MACs will range from about 1 mega bases to about 10 mega bases. They can also range from about 10 kb to about 30 mega bases bases. They can still further range from about 50 kb to about 12
15 mega bases or about 100 kb to about 10 mega bases or about 25 kb to about 500 kb or about 50 kb to about 250 kb or about 75 kb to about 200 kb or about 85 kb to about 150 kb.

Typically if the MACs are going to be shuttled between mammalian and bacterial cells they should be less than 300 kb in size. This type of MAC can also be
20 less than about 750 kb or about 600 kb or about 500 kb or about 400 kb or about 350 kb or about 250 kb or about 200 kb or about 150 kb. If the MACs are going to be shuttled between mammalian and yeast cells they are typically less than 1 mega base in size. This type of MAC can also be less than about 5 mega bases or about 2.5 mega bases or about 1.5 mega bases or about 900 kb or about 800 kb or about 700 kb or
25 about 600 kb or about 500 kb or about 400 kb or about 400 kb or about 200 kb or about 100 kb.

The size of the MACs is described in base pairs, but it is understood that unless otherwise stated, these numbers are not absolutes, but rather represent approximations of the sizes of the MACs. Thus, for each size of the MAC described it is understood
30 that this size could be "about" that size. There is little functional difference between a nucleic acid molecule of 1,500,000 bases and one that is 1,500, 342 bases. Those of

- 5 skill in the art understand that the sizes and ranges are given as direction, but do not necessarily functionally limit the MACs.

b) Form

The disclosed MACs can take a variety of forms. The form of the MAC refers to the shape of the artificial chromosome. The parts of the MAC that are required for
10 the MAC to function depend on the form that the MAC takes. Thus, is when designing MACs as disclosed it is important to be aware of what form the MAC will take inside of the target cell.

(1) Linear

MACs can be linear. A linear MAC is an artificial chromosome that has the
15 form or shape of a natural chromosome. This type of MAC has "ends" to the chromosome, much like most naturally occurring chromosomes. When a MAC is a linear MAC it must have telomeres. Telomeres are specialized purine rich sequences that are thought to protect the ends of a chromosome during replication, segregation, and mitosis. Telomere sequences and uses are well known in the art and are discussed
20 below.

(2) Circular

The disclosed MACs can also be circular. Circular MACs do not have a "beginning" or "ending," rather they are connected. There is no terminus to a circular MAC. When a MAC is circular, it does not need telomere sequence because there is no
25 end of the chromosome that must be protected during replication, segregation, and mitosis. A circular MAC may contain telomere sequence so that if it is linearized it can function as a linear MAC, but the telomere sequence is not required for the circular MAC to function.

5

c) Content

The content of the MACs is varied. The content can be characterized by sequence, requisite parts, size, and function. The content of the MACs depends on a number of things, for example, the form that the MACs will take, whether the MACs are going to be shuttled between bacterial and/or yeast cells, and the type of mammalian cell that the MAC will target. A general formula for the disclosed MACs is Y-X-Z-Y which represents the three parts of a MAC which must be required if the MAC is linear. If the MAC is circular, the formula for the required parts is X-Z. In this formula X represents an origin of replication. Z represents a centromeric region, or a region capable of ordering and segregating the artificial chromosome appropriately during a cell cycle. Y represents teleomeric sequence. When the MAC takes the form of a circular chromosome, Y is not required. Each of these parts has specific characteristics, properties, and requirements which are discussed below.

(1) Y-X-Z-Y

The Y-X-Z-Y nomenclature is used for ease of understanding of the structure of the MACs. While the functions provided by each part are necessary in each MAC or in each MAC their function must specifically be accounted for by, for example circularizing the MAC, the nomenclature is not intended to imply that the structure of the MAC always must be or arise from separate parts. If all of the functions are contained in one of the parts these MACs are an embodiment of the disclosed MACs. For example, as discussed in Example 1 the origin of replication and centromeric function are contained in the mammalian alphoid constructs used in the MACs and because the MACs are circular, they do not require a telomere sequence, but yet they function as MACs and these are considered an embodiment of the disclosed MACs.

5

(a) X part— origin of replication

In the Y-X-Z-Y formula for a MAC X represents an origin of replication. Origins of replication are regions of DNA from which DNA replication during the S phase of the cell cycle is primed. While the origins of replication, termed autonomously replicating sequence (ARS) are fully defined in yeast (Theis et al., *Proc. Natl. Acad. Sci. USA* 94: 10786-10791, 1997) there does not appear to be a specific corresponding origin of replication sequence in mammalian DNA. Grimes and Cooke, *Human Molecular Genetics*, 7(10):1635-1640 (1998) There are, however, numerous regions of mammalian DNA which can function as origins of replication. (Schlessinger and Nagaraja, *Ann. Med.*, 30:186-191 (1998); Dobbs et al., *Nucleic Acids Res.* 22:2479-89 (1994); and Aguinaga et al., *Genomics* 5:605-11 (1989)). It is known that for every 100 kb of mammalian DNA sequence there is a sequence that will support replication, but in practice sequences as short as 20 kb can support replication on episomal vectors. Calos, *Trends Genet.* 12:463-66 (1996). This data indicates that epigenetic mechanisms, such as CpG methylation patterning likely play some role in replication of DNA. Rein et al., *Mol. Cell. Biol.* 17:416-426 (1997).

(i) Size

The X-part of the disclosed MACs can be any size that supports replication of the MAC. One way of ensuring that the MAC has a functional X sequence is to require that the Y-X-Z-Y contain at least 5 kb of mammalian genomic DNA. In other embodiments the Y-X-Z-Y structure contains at least 10 kb, 15 kb, 20 kb, 25 kb, 30 kb, 35 kb, 40 kb, 45 kb, 50 kb, 60 kb, 70 kb, 80 kb, 90 kb, or 100 kb of mammalian genomic DNA. In general any region of mammalian DNA could be used as origin of replication. If you have replication of the MAC then the origin of replication is functioning as desired.

30

5

(ii) Source

The X-part of the Y-X-Z-Y MAC can be obtained from any number of sources of mammalian DNA. In general it can be any region of mammalian DNA that is not based on a repeat sequence, such as the alphoid DNA sequence

Typically an alphoid sequence of DNA does not have origins of replication in it, because the repeat sequences are so small, for example about 170 base pairs, and which can be repeated many times that there is not enough variation for the origin of replication sequences to be present. However, based on the disclosed compositions, these regions can function as origins of replication in mammalian, such human, cells.

(b) Z-part – centromere region

The Z-part of the Y-X-Z-Y MAC represents a centromere region. It is understood that a centromere region, broadly defines a functional stretch of nucleic acid that allows for segregation of the MAC during the cell cycle and during mitosis. This region can be isolated using the methods described herein, or can now be engineered based on the information obtained from the cloned natural centromere regions. For example, the centromere region can now be obtained from a Y chromosome or chromosome 22. It is understood that each chromosomal centromere region has unique properties, however, each region also has properties and structural features in common with the other centromeric regions. In some embodiments, the disclosed MACs contain Z-parts that are derived from specific centromeric regions, and in other configurations the MACs contain Z-parts that are made up of the common elements, shared between the centromeres isolated from different chromosomes. The Z-parts can be characterized by their size, by their content, function, and by their origin, for example.

5

(i) Source

One way to determine the size of the Z-part is to look at what gets cloned from specific centromeric regions. The Z-part is not limited to what is cloned from a centromeric region, but this is one way to describe and certainly to obtain the Z-part. For example, starting with the mini chromosome generated by Brown et al. (Brown et al., *Human Molec Gen.*, 3(8):1227-1237 (1994)) using one of the vectors disclosed herein alphoid regions derived from the Y chromosome have been isolated. Regions, of 250 kb, 170 kb, and 100 kb have been isolated.

Z-part regions have also been isolated from a number of other chromosomes. For example, regions have been isolated from chromosomes 2, 10, 11, 13, 15, 21, and 22. See Table 1. Table 1 characterizes, by size, YAC clones obtained with a disclosed TAR vector containing alphoid DNA as the targeting sequences. The clones were isolated by a TAR cloning system based on a counter-selectable marker as described in Figure 1 and Example 1. Table 1 shows that the regions isolated from the various chromosomal centromeres can vary in size. For example, various size fragments from a centromeric region of the chromosome 22 have been isolated. These fragments either contain different size blocks of alphoid DNA or alphoid DNA and non-alphoid DNA from pericentromeric regions. Isolation of YACs containing different regions of a centromere would allow to clarify what sequences are critical for efficient MAC formation

25

5 Table 1

Characterization of YAC Clones Obtained with a TAR Vector Containing
Alphoid DNA as Targeting Sequences

YAC	SIZE	FISH	YAC end Sequences	BAC size
Chr22#3	50kb	Nd		50kb
Chr22#5	140kb	chr22/CEN	3-5 satellites (EcoR1)	80kb
Chr22#6	120kb	chr22/CEN		120kb
Chr22#9	90kb, 170kb	chr22/CEN		110kb
Chr22#10	80kb	nd		80kb
Chr22#11	60kb, 140kb	chr22/CEN		140kb
Chr22#14	50kb, 100kb, 200kb	chr22/CEN		70kb
Chr22#15	100kb	chr22/CEN		100kb
Chr22#19	70kb	chr22/CEN		110kb
Chr22#20	60kb	nd		60kb
Chr22#29	70kb, 200kb	chr22/CEN	3-4 satellites (EcorR1)	180kb
Chr22#35	60kb	chr22/CEN		60kb
Chr22#11	60kb, 100kb	chr22/CEN		100kb
Chr11#2	75kb, 150kb, 400kb	chr11/CEN	4-3 satellites (EcorR1)	150kb
MRC5#8	75kb	nd		nd
MRC5#11	140kb	chr8/CEN		120kb
MRC5#13	140kb, 220kb, 270kb	chr13, 21/CEN	2-2 satellites (EcoR1)	140kb
MRC5#16	90kb	nd		nd
MRC5#25	220kb	chr2/CEN		220kb
MRC5#26	140kb	chr15/CEN		120kb
MRC5#41	120kb	nd		nd
MRC5#59	150kb	chr5/CEN, 19/CEN		150kb

10

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(ii) Size

The size of the Z-part can range from very small (for example about 1.6 kb) to very large (for example, about 500 kb). The size of the Z-part is determined by whether the Z-part is capable of causing the MAC to appropriately segregate the MAC during the cell cycle.

10 The size of the Z-part can range from about 170b to about 10mega bases. The size of the Z-part can range from about 1.6 kb to about 4 kb, 2.8 kb to about 4 mega bases, 2.9 kb to about 4 mega bases, 5.7 mega bases to about 4 mega bases, 20 kb to about 1 mega base , 40 kb to about 1 mega base kb, 60 kb to about 1 mega base . In some embodiments the ranges can be from about 70 kb to about 200 kb, about 250 kb
 15 to about 600 kb, or about 150 kb to about 300 kb, or from about 100 to 250 kb. In some embodiments the Z-part can be less than or equal to about 300 kb between because MACs of such size can be shuttled between bacterial, yeast and mammalian and can be used as a gene delivery system. In some embodiments the MACs are less than or equal to about 550 kb or about 500 kb or about 450 kb or about 400 kb or about 350 kb or
 20 about 300 kb or about 250 kb or about 225 kb or about 200 kb or about 175 kb or about 150 kb or about 125 kb or about 100 kb or about 95 kb or about 90 kb or about 85 kb or about 80 kb or about 75 kb or about 70 kb or about 65 kb or about 60 kb or about 55 kb or about 50 kb or about 45 kb or about 40 kb or about 35 kb or about 30 kb or about 25 kb or about 20 kb or about 15 kb or about 10 kb or about 5 kb. In some embodiments,
 25 the Z-part is about 600 kb, about 300 kb, about 260 kb, about 250 kb, about 240 kb, about 200 kb, about 150 kb, about 140 kb, about 100 kb, or about 70 kb.

(iii) Content

Another way of characterizing the Z-part of the Y-X-Z-Y MAC is by the content of the Z-part. By content is meant the sequence or other structural attributes
 30 that define the Z-part. The Z-parts in some embodiments contain aliphoid DNA in

5 general, and in other embodiments contain specific alphoid regions, unique to the particular chromosome they were isolated from. The Z-part could also contain alphoid DNA sequences along with non-alphoid DNA incorporated into alphoid DNA arrays.

(a) Alphoid DNA

Alphoid DNA refers to DNA that is present near all known mammalian
 10 centromeres. Alphoid DNA is highly repetitive DNA, and it is made up generally of alpha satellite DNA. Alphoid DNA is typically AT rich DNA and also typically contains CENPB protein binding sites. (Barry et al. *Human Molecular Genetics*, 8(2):217-227 (1999); Ikeno et al., *Nature Biotechnology*, 16:431-39 (1998)). While the alphoid DNA of each chromosome has common attributes, each chromosomal
 15 centromere also has unique features. For example alphoid DNA of the human chromosome 22 consists of two units 2.1 kb and 2.8 kb. These units can be identify by EcoRI digestion. In the human Y chromosome alphoid DNA arrays consists off two different size units, 2.8 kb and 2.9 kb that can be identified by SpeI digestion.

(b) Chromosome Y alphoid DNA

20 The centromere defined as $\Delta Yq74$ is the alphoid centromeric region that was isolated from the mini chromosome constructed by Brown et al. *Human Molec Gen.*, 3(8):1227-1237 (1994). The isolation and characterization of this region are described in Example 1. This region has a number of attributes, such as inverted repeats and a lack of any consensus CENP-B protein binding sites.

25

(1) Macrostructure

The chromosome Y centromeric region is made up of two repeating units where each repeating unit is represented by a 2950 bp fragment (SEQ ID NO:3 and Figure 7) and a 2847 bp fragment (SEQ ID NO:2 and Figure 8) (Figure 2.). As discussed in Example 1, these fragments that make up the macrostructure of the
 30 repeating unit of the chromosome Y alphoid DNA are determined by a Spe I digestion

5 of the isolated alphoid DNA. In the centromeric region each unit is repeated 23 times forming a 140 kb alphoid DNA array. The units are organized as tandem repeats. Each of these fragments itself is made up of a smaller divergent repeating unit. This repeating unit is about 170 bases long and is described in detail below. The number of repeating units may vary and is ultimately dependent on the structure needed for appropriate segregation of the HACs. In some embodiments the repeating unit may be as small as one of the specific alpha satellite monomers, and in other embodiments, for example, the size may correspond to one of the major Spe I fragments, such as the 2.8kb or 2.9 kb fragments. As discussed herein these characteristics may be applicable for other alphoid satellite and centromeric regions, and this is most appropriately determined by the functions of these regions as discussed.

4 Y chromosome alpha satellite structure

The macrostructure of the Y chromosome centromeric region is made up of a smaller alpha satellite region that is about 170 base pairs. Specifically, one 2950 bp fragment and one 2847 bp fragment in that order are made up of 34 variants of the about 170 bp alpha satellite region. These alpha satellites are number 1-34 and the specific sequence of each of these satellites is shown as SEQ ID NOs: 4-37 respectively and are also shown in comparative form in Figure 3 and in Figure 5A. The identity of these sequences amongst each other can be determined by tabulating the variations and similarities of the various sequences. The variation within the sequences represents the divergence that has taken place within these regions.

Identity to the chromosome Y sequences

In one embodiment of the MACs, the Z-part of the Y-X-Z-Y MACs is defined by specific levels of identity to the specific alpha satellites defined by SEQ ID NOs: 4-37. For example, in some embodiments the Z-part can have or be greater than or equal to about 99.99%, about 99.95% identity, about 99.90% identity, about 99.80% identity, about 99.70% identity, about 99.60% identity, about 99.50% identity, about

5 99.40% identity, about 99.30% identity, about 99.20% identity, about 99.10% identity, about 99.00 % identity, about 98.00 % identity, about 97.00 % identity, about 96.00 % identity, about 95.00 % identity, about 94.00 % identity, about 93.00 % identity, about 92.00 % identity, about 91.00 % identity, about 90.00 % identity, about 85.00 % identity, or about 80.00 % identity to any of SEQ ID NO:1-46 or 51-56. The identity
 10 of sequences can be compared by looking at the sequence of a given molecule and then comparing it to the sequence of choice, disclosed herein, for example in Figures 3 and 5. Embodiments of the disclosed MACs specifically include identities that are greater than about the specific recitations of homology between certain disclosed alpha satellite regions in Figure 5. For example, Figure 5 discloses that there is 77.0%
 15 homology between alpha satellites 3 and 27, 89.4% homology between alpha satellites 17 and 21. Therefore, MACs having identities of about 89.4% and about 77.0% to SEQ ID NOs:4-37 are disclosed. Also it is understood that the sequence variation between the alpha satellite regions, SEQ ID NOs:4-37, 53 and 54 can be carried through to the larger repeat units that make up the Z-part of the MAC.

20

*1.6 kb structure of $\Delta Yq74$
 having Inverted repeats*

The macrostructure defined by the 2847-2950 repeating unit which can be isolated by a Spe I digestion of the isolated $\Delta Yq74$ region is the dominant structure that is present. A minor Spe I product that is shown in Figure 4 and represented by SEQ ID
 25 NO:1 is approximately 1800 bases long. (The fragment moves as 1.6 kb fragment during electrophoresis. An abnormal mobility of the fragment is explained by the presence of palindromic sequence) This minor 1.6 kb fragment contains specific alpha satellite DNA also, but rather than having the alpha satellites arranged in a tandem array as the major repeating unit does, the minor fragment has 6 full alpha satellite
 30 repeats which are in tandem and 3 which are inverted repeats. The variation between these repeats can also be defined and each individual repeat is defined in SEQ ID NOs: 38-46. Because this fragment was not detected in normal (i.e. non truncated) chromosome Y, the fragment arose during truncation of the chromosome. It is known

5 that chromosome truncation is often accompanied by rearrangement of the targeted region. These rearrangements occurred near the end of an alphoid DNA array.

No CENP-B boxes

The chromosome Y centromeric DNA region as well as large blocks of alphoid DNA from chromosome 22 do not have any CENP-B boxes. CENP-B boxes are
10 specific DNA binding sites for the DNA binding protein, CENP-B (Masumoto et al., J. Cell Biol., 109:1963-1973 (1998)). It has been suggested that CENP-B boxes are necessary for centromere function, however, as disclosed here MACs containing the disclosed centromere regions can function without these binding DNA binding protein sites. Thus, in some embodiments the Z-part of the Y-X-Z-Y MAC does not require a
15 functional CENP-B protein binding site, which can be obtained by not having the sequence described as a CENP-B site in the literature.

(c) Other centromeres

The Z-part can also be derived from the centromeric regions of other chromosomes. These centromere regions can be isolated using the methods and vectors
20 discussed in the Examples.

Also disclosed is the isolation of alphoid DNA arrays from non-Y based human chromosomes by TAR cloning. A TAR cloning strategy has also been applied for the isolation of centromeric DNAs from several human chromosomes including chromosome 22, 11, 2, 15, and 13. Consensus alphoid DNA sequences or
25 chromosome-specific alphoid DNA sequences were included into a TAR vector as targeting sequences (hooks). Isolation was highly selective and specific when a SUP11-based counter-selectable marker was included into the TAR vector. Isolation of chromosome-specific alphoid DNA arrays was confirmed by in situ hybridization and restriction analysis of YAC/BAC isolates. Fig. 13 and 15 show FISH mapping of
30 YACs containing alphoid DNA from two human chromosomes, (chromosome 15 and chromosome 22). Physical mapping data were further confirmed by detailed restriction

5 analysis. An alphoid DNA array of each human chromosome exhibits a specific restriction pattern due to the presence of a chromosome-specific alphoid DNA unit. For example, for chromosome 11 this unit is a 0.8 kb fragment that can be identified by Xba I digestion. For chromosome 2 the unit is a 0.68 kb fragment that can be identified by Xba I digestion. For chromosome 13 the unit is a 3.9 kb fragment that can be
10 identified by Hind III digestion. In the human chromosome 22 there are two units, 2.1 kb and 2.8 kb in size. These units can be identified by EcoRI digestion. Figure 15 shows digestion of YAC/BACs isolated from chromosome 22 by EcoRI. The restriction profile is specific for chromosome 22, indicating that a TAR cloning procedure provides a powerful tool for selective cloning of centromeric regions. Any
15 of these YAC/BAC isolates can be used for construction of MACs.

In some embodiments alphoid arrays which are derived from either human chromosome 17 or human chromosome 21 are not included in the Z-part of the disclosed MACs. In other embodiments, chromosomes that lack a CENP-B protein binding site are included, and thus, human chromosome 17 and 21 alphoid arrays
20 lacking a CENP-B protein binding site are included, when they function as the disclosed MACs.

The Z-part of the MAC can also be further defined by the function that it performs. This function is related to the appropriate segregation of the MAC of which it is a part during mitosis. Proper segregation is a main function of the centromere.
25 This segregation results in a maintenance of MAC as an extrachromosomal element in a single copy number in transfected cells. Formation of MACs can be detected either by FISH (as an additional chromosome on the metaphase plate) or by immunofluorescence using kinetohore-specific antibodies. Alternatively the MAC can be rescued by E. coli or yeast transformation if the MAC contains YAC and BAC
30 cassettes.

5 The main function of the Z-part is to be provide a centromere like activity to the
MACs, which means that the MACs are able to appropriately replicate and segregate.
Also disclosed, however, are embodiments where the Z-part is also functioning as an
origin of replication, i.e. the X-part. Thus, as discussed in the examples, the disclosed
10 alphoid regions, particularly the alphoid regions isolated from the Y chromosome and
chromosome 22 can function without a separate origin of replication, or in other words
can function as an origin of replication in mammalian cells.

(c) Y part – telomeres

 The Y-part of the Y-X-Z-Y MAC represents the telomere region. Telomeres
are regions of DNA which help prevent the unwanted degradation of the termini of
15 chromosomes. The teleomere is a highly repetitive sequence that varies from organism
to organsim. For example, in mammals the most frequent telomere sequence repeat is
(TTAGGG)_n and the repeat structures can be from for example 2-20 kb. The following
publications and patents discuss telomeres, telomerase and methods and reagents
related to telomers: United States Patent Nos. 6,093,809, 6,007,989, 5,695,932,
20 5,645,986, 4,283,500 which are herein incorporated by reference.

(2) additions

 The MACs in addition to the required parts, such as a centromere type region
and a sequence capable of being replicated can include other sequences. In this
situation the MAC is acting much like a vector, as a vehicle for delivery and expression
25 of exogenous DNA in a cell. The added benefit of the disclosed MACs is that they are
stably replicated and propagated with the dividing cell. Thus there are a number of
additions that be added onto the MACs which either provide a new use for the MAC or
which aid in the use of the MAC. A few non-limiting examples of these types of
additions are Marker regions, transgenes, and tracking motifs.

5

(a) Markers

The MACs can include nucleic acid sequence encoding a marker product. This marker product is used to determine if the MAC has been delivered to the cell and once delivered is being expressed. Examples of marker genes are the E. Coli lacZ gene which encodes b-galactosidase and green fluorescent protein.

- 10 In some embodiments the marker may be a selectable marker. Examples of suitable selectable markers for mammalian cells are dihydrofolate reductase (DHFR), thymidine kinase, neomycin, neomycin analog G418, hydromycin, and puromycin. When such selectable markers are successfully transferred into a mammalian host cell, the transformed mammalian host cell can survive if placed under selective pressure.
- 15 There are two widely used distinct categories of selective regimes. The first category is based on a cell's metabolism and the use of a mutant cell line which lacks the ability to grow independent of a supplemented media. Two examples are: CHO DHFR- cells and mouse LTK- cells. These cells lack the ability to grow without the addition of such nutrients as thymidine or hypoxanthine. Because these cells lack certain genes
- 20 necessary for a complete nucleotide synthesis pathway, they cannot survive unless the missing nucleotides are provided in a supplemented media. An alternative to supplementing the media is to introduce an intact DHFR or TK gene into cells lacking the respective genes, thus altering their growth requirements. Individual cells which were not transformed with the DHFR or TK gene will not be capable of survival in
- 25 non-supplemented media.

The second category is dominant selection which refers to a selection scheme used in any cell type and does not require the use of a mutant cell line. These schemes typically use a drug to arrest growth of a host cell. Those cells which have a novel gene would express a protein conveying drug resistance and would survive the selection.

- 30 Examples of such dominant selection use the drugs neomycin, (Southern P. and Berg, P., J. Molec. Appl. Genet. 1: 327 (1982)), mycophenolic acid, (Mulligan, R.C. and Berg, P. Science 209: 1422 (1980)) or hygromycin, (Sugden, B. et al., Mol. Cell. Biol.

5 5: 410-413 (1985)). The three examples employ bacterial genes under eukaryotic control to convey resistance to the appropriate drug G418 or neomycin (geneticin), xgpt (mycophenolic acid) or hygromycin, respectively. Others include the neomycin analog G418 and puramycin.

The use of Markers can be tailored for the type of cell that the MAC is in and
10 for the type of organism the MAC is in. For example, if the MAC is to be a MAC which can shuttle between bacterial and yeast cells as well as mammalian cells, it may be desirable to engineer a Marker specific for the bacterial cell, for the yeast cell, and for the mammalian cell. Those of skill in the art, given the disclosed MACs are capable of selecting and using the appropriate Marker for a given set of conditions or a given
15 set of cellular requirements.

The Markers can be useful in tracking the MAC through cell types and to determine if the MAC is present and functional in different cell types. The Markers can also be useful in tracking any changes that may take place in the MACs of over time or over a number of cell cycle generations.

20

(b) Transgenes

The transgenes that can be placed into the disclosed MACs can encode a variety of different types of molecules. For example, these transgenes can encode genes which will be expressed and produce a protein product or they can encode an RNA molecule that when it is expressed will encode functional nucleic acid, such as a ribozyme.

25

Functional nucleic acids are nucleic acid molecules that have a specific function, such as binding a target molecule or catalyzing a specific reaction. Functional nucleic acid molecules can be divided into the following categories, which are not meant to be limiting. For example, functional nucleic acids include antisense molecules, aptamers, ribozymes, triplex forming molecules, and external guide
30 sequences. The functional nucleic acid molecules can act as effectors, inhibitors,

5 modulators, and stimulators of a specific activity possessed by a target molecule, or the functional nucleic acid molecules can possess a de novo activity independent of any other molecules.

Functional nucleic acid molecules can interact with any macromolecule, such as DNA, RNA, polypeptides, or carbohydrate chains. Thus, functional nucleic acids can
10 interact with a target mRNA of the host cell or a target genomic DNA of the host cell or a target polypeptide of the host cell. Often functional nucleic acids are designed to interact with other nucleic acids based on sequence homology between the target molecule and the functional nucleic acid molecule. In other situations, the specific recognition between the functional nucleic acid molecule and the target molecule is not
15 based on sequence homology between the functional nucleic acid molecule and the target molecule, but rather is based on the formation of tertiary structure that allows specific recognition to take place.

Antisense molecules are designed to interact with a target nucleic acid molecule through either canonical or non-canonical base pairing. The interaction of the antisense
20 molecule and the target molecule is designed to promote the destruction of the target molecule through, for example, RNaseH mediated RNA-DNA hybrid degradation. Alternatively the antisense molecule is designed to interrupt a processing function that normally would take place on the target molecule, such as transcription or replication. Antisense molecules can be designed based on the sequence of the target molecule.
25 Numerous methods for optimization of antisense efficiency by finding the most accessible regions of the target molecule exist. Exemplary methods would be in vitro selection experiments and DNA modification studies using DMS and DEPC. It is preferred that antisense molecules bind the target molecule with a dissociation constant (k_d) less than 10^{-6} . It is more preferred that antisense molecules bind with a k_d less than
30 10^{-8} . It is also more preferred that the antisense molecules bind the target molecule with a k_d less than 10^{-10} . It is also preferred that the antisense molecules bind the target molecule with a k_d less than 10^{-12} . A representative sample of methods and techniques

- 5 which aid in the design and use of antisense molecules can be found in the following non-limiting list of United States patents: 5,135,917, 5,294,533, 5,627,158, 5,641,754, 5,691,317, 5,780,607, 5,786,138, 5,849,903, 5,856,103, 5,919,772, 5,955,590, 5,990,088, 5,994,320, 5,998,602, 6,005,095, 6,007,995, 6,013,522, 6,017,898, 6,018,042, 6,025,198, 6,033,910, 6,040,296, 6,046,004, 6,046,319, and 6,057,437,
- 10 which are herein incorporated by reference.

- Aptamers are molecules that interact with a target molecule, preferably in a specific way. Typically aptamers are small nucleic acids ranging from 15-50 bases in length that fold into defined secondary and tertiary structures, such as stem-loops or G-quartets. Aptamers can bind small molecules, such as ATP (United States patent
- 15 5,631,146, herein incorporated by reference) and theophiline (United States patent 5,580,737, herein incorporated by reference), as well as large molecules, such as reverse transcriptase (United States patent 5,786,462, herein incorporated by reference) and thrombin (United States patent 5,543,293, herein incorporated by reference). Aptamers can bind very tightly with k_d s from the target molecule of less than 10⁻¹² M.
- 20 It is preferred that the aptamers bind the target molecule with a k_d less than 10⁻⁶. It is more preferred that the aptamers bind the target molecule with a k_d less than 10⁻⁸. It is also more preferred that the aptamers bind the target molecule with a k_d less than 10⁻¹⁰. It is also preferred that the aptamers bind the target molecule with a k_d less than 10⁻¹². Aptamers can bind the target molecule with a very high degree of specificity. For
- 25 example, aptamers have been isolated that have greater than a 10000 fold difference in binding affinities between the target molecule and another molecule that differ at only a single position on the molecule (United States patent 5,543,293, herein incorporated by reference). It is preferred that the aptamer have a k_d with the target molecule at least 10 fold lower than the k_d with a background binding molecule. It is more preferred that
- 30 the aptamer have a k_d with the target molecule at least 100 fold lower than the k_d with a background binding molecule. It is more preferred that the aptamer have a k_d with the target molecule at least 1000 fold lower than the k_d with a background binding molecule. It is preferred that the aptamer have a k_d with the target molecule at least

5 10000 fold lower than the k_d with a background binding molecule. It is preferred when doing the comparison for a polypeptide for example, that the background molecule be a different polypeptide. Representative examples of how to make and use aptamers to bind a variety of different target molecules can be found in the following non-limiting list of United States patents: 5,476,766, 5,503,978, 5,631,146, 5,731,424, 5,780,228,
10 5,792,613, 5,795,721, 5,846,713, 5,858,660, 5,861,254, 5,864,026, 5,869,641, 5,958,691, 6,001,988, 6,011,020, 6,013,443, 6,020,130, 6,028,186, 6,030,776, and 6,051,698, which are herein incorporated by reference.

Ribozymes are nucleic acid molecules that are capable of catalyzing a chemical reaction, either intramolecularly or intermolecularly. Ribozymes are thus catalytic
15 nucleic acid. It is preferred that the ribozymes catalyze intermolecular reactions. There are a number of different types of ribozymes that catalyze nuclease or nucleic acid polymerase type reactions which are based on ribozymes found in natural systems, such as hammerhead ribozymes, (for example, but not limited to the following United States patents: 5,334,711, 5,436,330, 5,616,466, 5,633,133, 5,646,020, 5,652,094, 5,712,384,
20 5,770,715, 5,856,463, 5,861,288, 5,891,683, 5,891,684, 5,985,621, 5,989,908, 5,998,193, 5,998,203, WO 9858058 by Ludwig and Sproat, herein incorporated by reference, WO 9858057 by Ludwig and Sproat, herein incorporated by reference, and WO 9718312 by Ludwig and Sproat, herein incorporated by reference) hairpin ribozymes (for example, but not limited to the following United States patents:
25 5,631,115, 5,646,031, 5,683,902, 5,712,384, 5,856,188, 5,866,701, 5,869,339, and 6,022,962, which are herein incorporated by reference), and tetrahymena ribozymes (for example, but not limited to the following United States patents: 5,595,873 and 5,652,107, which are herein incorporated by reference). There are also a number of ribozymes that are not found in natural systems, but which have been engineered to
30 catalyze specific reactions de novo (for example, but not limited to the following United States patents: 5,580,967, 5,688,670, 5,807,718, and 5,910,408, which are herein incorporated by reference). Preferred ribozymes cleave RNA or DNA substrates, and more preferably cleave RNA substrates. Ribozymes typically cleave

5 nucleic acid substrates through recognition and binding of the target substrate with subsequent cleavage. This recognition is often based mostly on canonical or non-canonical base pair interactions. This property makes ribozymes particularly good candidates for target specific cleavage of nucleic acids because recognition of the target substrate is based on the target substrates sequence. Representative examples of how to
10 make and use ribozymes to catalyze a variety of different reactions can be found in the following non-limiting list of United States patents: 5,646,042, 5,693,535, 5,731,295, 5,811,300, 5,837,855, 5,869,253, 5,877,021, 5,877,022, 5,972,699, 5,972,704, 5,989,906, and 6,017,756, which are herein incorporated by reference.

Triplex forming functional nucleic acid molecules are molecules that can
15 interact with either double-stranded or single-stranded nucleic acid. When triplex molecules interact with a target region, a structure called a triplex is formed, in which there are three strands of DNA forming a complex dependant on both Watson-Crick and Hoogsteen base-pairing. Triplex molecules are preferred because they can bind target regions with high affinity and specificity. It is preferred that the triplex forming
20 molecules bind the target molecule with a k_d less than 10^{-6} . It is more preferred that the triplex forming molecules bind with a k_d less than 10^{-8} . It is also more preferred that the triplex forming molecules bind the target molecule with a k_d less than 10^{-10} . It is also preferred that the triplex forming molecules bind the target molecule with a k_d less than 10^{-12} . Representative examples of how to make and use triplex forming molecules to
25 bind a variety of different target molecules can be found in the following non-limiting list of United States patents: 5,176,996, 5,645,985, 5,650,316, 5,683,874, 5,693,773, 5,834,185, 5,869,246, 5,874,566, and 5,962,426, which are herein incorporated by reference.

External guide sequences (EGSs) are molecules that bind a target nucleic acid
30 molecule forming a complex, and this complex is recognized by RNase P, which cleaves the target molecule. EGSs can be designed to specifically target a RNA molecule of choice. RNase P aids in processing transfer RNA (tRNA) within a cell.

5 Bacterial RNase P can be recruited to cleave virtually any RNA sequence by using an EGS that causes the target RNA:EGS complex to mimic the natural tRNA substrate. (WO 92/03566 by Yale, and Forster and Altman, Science 238:407-409 (1990), which are herein incorporated by reference).

Similarly, eukaryotic EGS/RNase P-directed cleavage of RNA can be utilized
10 to cleave desired targets within eukaryotic cells. (Yuan et al., Proc. Natl. Acad. Sci. USA 89:8006-8010 (1992); WO 93/22434 by Yale; WO 95/24489 by Yale; Yuan and Altman, EMBO J 14:159-168 (1995), and Carrara et al., Proc. Natl. Acad. Sci. (USA) 92:2627-2631 (1995), which are herein incorporated by reference). Representative
15 examples of how to make and use EGS molecules to facilitate cleavage of a variety of different target molecules be found in the following non-limiting list of United States patents: 5,168,053, 5,624,824, 5,683,873, 5,728,521, 5,869,248, and 5,877,162, which are herein incorporated by reference.

The transgenes can also encode proteins. These proteins, can either be native to the organism or cell type, or they can be exogenous. Typically, for example, if the
20 transgene encodes a protein, it may be protein related to a certain disease state, wherein the protein is underproduced or is non-functional when produced from the native gene. In this situation, the protein encoded by the MAC is meant as a replacement protein. In other situations, the protein may be non-natural, meaning that it is not typically expressed in the cell type or organism in which the MAC is found. An example of this
25 type of situation, may be a protein or small peptide that acts as mimic or inhibitor or inhibitor of a target molecule which is unregulated in the cell or organism possessing the MAC.

(c) Control sequences

The transgenes, or other sequences, in the MACs can contain promoters, and/or
30 enhancers to help control the expression of the desired gene product or sequence. A promoter is generally a sequence or sequences of DNA that function when in a

- 5 relatively fixed location in regard to the transcription start site. A promoter contains core elements required for basic interaction of RNA polymerase and transcription factors, and may contain upstream elements and response elements.

(i) Viral Promoters and Enhancers

Preferred promoters controlling transcription from vectors in mammalian host
10 cells may be obtained from various sources, for example, the genomes of viruses such as: polyoma, Simian Virus 40 (SV40), adenovirus, retroviruses, hepatitis-B virus and most preferably cytomegalovirus, or from heterologous mammalian promoters, e.g. beta actin promoter. The early and late promoters of the SV40 virus are conveniently obtained as an SV40 restriction fragment which also contains the SV40 viral origin of
15 replication (Fiers et al., Nature, 273: 113 (1978)). The immediate early promoter of the human cytomegalovirus is conveniently obtained as a HindIII E restriction fragment (Greenway, P.J. et al., Gene 18: 355-360 (1982)). Of course, promoters from the host cell or related species also are useful herein.

Enhancer generally refers to a sequence of DNA that functions at no fixed
20 distance from the transcription start site and can be either 5' (Laimins, L. et al., Proc. Natl. Acad. Sci. 78: 993 (1981)) or 3' (Lusky, M.L., et al., Mol. Cell Bio. 3: 1108 (1983)) to the transcription unit. Furthermore, enhancers can be within an intron (Banerji, J.L. et al., Cell 33: 729 (1983)) as well as within the coding sequence itself (Osborne, T.F., et al., Mol. Cell Bio. 4: 1293 (1984)). They are usually between 10
25 and 300 bp in length, and they function in cis. Enhancers function to increase transcription from nearby promoters. Enhancers also often contain response elements that mediate the regulation of transcription. Promoters can also contain response elements that mediate the regulation of transcription. Enhancers often determine the regulation of expression of a gene. While many enhancer sequences are now known
30 from mammalian genes (globin, elastase, albumin, -fetoprotein and insulin), typically one will use an enhancer from a eukaryotic cell virus. Preferred examples are the SV40

5 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

The promotor and/or enhancer may be specifically activated either by light or specific chemical events which trigger their function. Systems can be regulated by reagents such as tetracycline and dexamethasone. There are also ways to enhance viral vector gene expression by exposure to irradiation, such as gamma irradiation, or alkylating chemotherapy drugs.

The promoter and/or enhancer region act as a constitutive promoter and/or enhancer to maximize expression of the region of the transcription unit to be transcribed. It is further preferred that the promoter and/or enhancer region be active in all eukaryotic cell types. A preferred promoter of this type is the CMV promoter (650 bases). Other promoters are SV40 promoters, cytomegalovirus (full length promoter), and retroviral vector LTF.

It has been shown that specific regulatory elements can be cloned and used to construct expression vectors that are selectively expressed in specific cell types such as melanoma cells. The glial fibrillary acidic protein (GFAP) promoter has been used to selectively express genes in cells of glial origin.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human or nucleated cells) may also contain sequences necessary for the termination of transcription which may affect mRNA expression. These regions are transcribed as polyadenylated segments in the untranslated portion of the mRNA encoding tissue factor protein. The 3' untranslated regions also include transcription termination sites. It is preferred that the transcription unit also contain a polyadenylation region. One benefit of this region is that it increases the likelihood that the transcribed unit will be processed and transported like mRNA. The identification and use of polyadenylation signals in expression constructs is well established. It is

5 preferred that homologous polyadenylation signals be used in the transgene constructs.
In one embodiment of the transcription unit, the polyadenylation region is derived
from the SV40 early polyadenylation signal and consists of about 400 bases. It is also
preferred that the transcribed units contain other standard sequences alone or in
combination with the above sequences improve expression from, or stability of, the
10 construct.

d) Function

The disclosed MACs can further be characterized by their function. The MACs
should be able to both replicate and segregate normally during a cell cycle i.e. MAC
should be mitotically stable. MACs should be maintained in a single copy number in a
15 transfectant cell. There should be no inhibition of expression of genes cloned in MACs
MACs should not integrate into mammalian chromosomes. The MACs also can
optionally have a number of other functional properties.

(1) Can shuttle between BAC, YAC, and MAC

One beneficial property that the disclosed MACs can possess is the ability to be
20 shuttled back and forth between mammalian, bacterial, and yeast cells. The MACs that
have this property will have specialized structural features that for example, allow for
replication in all three types of cells. For example, DNA sequence that has origins of
replication sufficient to promote replication in mammalian cells will typically not
support replication in yeast cells. Yeast cells typically require ARS sequences for
25 replication. In contrast to other MACs, the disclosed MACs contain cryptic ARS
sequences present within alphoid DNA array (Figure 23). The ability to shuttle between
these three different organisms allows for a broad range of recombinant biology
manipulations that would not be present or as easily realized if the MACs only
functioned in mammalian cells. For example, homologous recombination techniques,
30 available in yeast, but not typically available in mammalian cells, can be performed on

5 a MAC that can be shuttled back and forth between a yeast cell and a mammalian cell. For example, an alphoid DNA array can be modified by homologous recombination in yeast (deletions of one type of units or insertion of another type of units) to study a function of centromere. Moreover, a transgene cloned in a MAC could be mutated by homologous recombination in yeast to study a gene expression.

10 Typically MACs capable of shuttling between bacterial, yeast, and mammalian cells will be circular or possess the ability to be circularized and linearized by discreet manipulations of the MAC. Linear pieces of DNA do not replicate well in bacterial or yeast cells. A linear MAC can be engineered so that it can be circularized. Such circularization can be easily carried out by homologous recombination in yeast
 15 similar to that has been done for linear YACs (Cocchia et al. Nucl. Acids Res.28:E81, 2000.). Alternatively the circularization could be induced using Lex-Cre site-specific recombination system (Qin et al., Nucl. Acids Res. 23: 1923-1927.)

(2) Does not increase size when amplified

Another beneficial property that the MACs can possess is the ability to maintain
 20 there size and structure when being shuttled between bacterial, yeast, and mammalian cells. This property is due in part to the high divergence that can exist in the alpha satellite regions of the disclosed Z-part of the MAC. In certain constructs, the greater the internal homology, the greater the chance that homologous recombination events can arise in the host yeast cell, for example. Especially in yeast and bacteria, the more
 25 divergent the sequences the more stable the MAC will be in yeast and bacteria. Thus, variation between the alpha satellites that make up the Z-part of the MAC can be a desirable goal.

5 (3) Can carry transgenes

As discussed the disclosed MACs can optionally carry a variety of transgenes which are discussed below. These transgenes can perform a variety of functions, including but not limited to, the delivery of some type of pharmaceutical product, the delivery of some type of tool which can be used for the study of cellular function or the
10 cell cycle.

2. Shuttle vectors

The basic TAR cloning vector pVC-ARS is a derivative of the Bluescript-based yeast-*E. coli* shuttle vector pRS313 (Sikorski and Hieter, Genetics 122:19-27,1989). This plasmid contains a yeast origin of replication (*ARSH4*) from pRS313. pVC604
15 has an extensive polylinker consisting of 14 restriction endonuclease 6- and 8 bp recognition sites for flexibility in cloning of particular fragments of interest.

The functional DNA segments of the plasmid are indicated as follows: *CEN6* = a 196 bp fragment of the yeast centromere VI; *HIS3* = marker for yeast cells; *Amp^R* = ampicilline-resistance gene. This part of the vector allows it to be cloned and to
20 propagate human DNA inserts as YACs. Construction of a TAR vector for isolation of centromeric regions includes cloning of short specific alphoid DNA sequences (hooks) and a counter-selectable marker SUP11.

Other counter-selectable markers could be other yeast suppressor t-RNA genes or genes that are toxic for yeast (for example a gene encoding a killer-factor toxin.
25 (Suzuki et al. Protein Eng. 13:73-76, 2000.). These genes could be used in the same way to achieve the same result. Those of skill in the art can readily supply this part of the shuttle vector, and they can determine if the SUP11 substitute is functioning as the disclosed vectors and MACs.

5

To propagate isolated centromeric DNAs in *E. coli* cells a set of retrofitting vectors is disclosed. A typical retrofitting vector contains two short (approximately 300 bp each) targeting sequences, A and B, flanking the *ColE1* origin of replication and the *Amp^R* gene in the pVC604-based TAR cloning vectors (Kouprina et al., Proc. Natl. Acad. Sci. USA 95: 4469-4474, 1998). These targeting sequences are separated by a unique *Bam*HI site. Recombination of the vector with a YAC during yeast transformation creates the shuttle vector construct: following the recombination event, the *ColE1* origin of replication in the TAR cloning vector is replaced by a cassette containing the *F*-factor origin of replication, the chloramphenicol acetyltransferase (*Cm^R*) gene, a mammalian genetic marker and the *URA3* yeast selectable marker. The presence of a mammalian marker (such as *Neo^R* gene or HygroR gene or BsdR gene) allows for the selection of the construct during transfection into mammalian cells. There are numerous other yeast markers that can be substituted for the specific markers disclosed, and as discussed herein the functionality of these substitutions can be determined. Some embodiments will incorporate these substitutions as long as they retain the desired property of the various MACs and shuttle vectors disclosed herein.

It is understood that the shuttle vectors have the properties of either shuttling between yeast and mammalian cells, such as human cells, or yeast and bacteria cells, or mammalian cells, such as human and bacteria cells, or between all three different sets of cells. The cloning vectors which are described herein often are designed so that they can be shuttle vectors as well as cloning vectors. Thus, there are parts of shuttle vectors in general and the disclosed cloning vectors that can be similar or the same. However, it is specifically contemplated that the shuttle vectors can be engineered such that they do not have the any parts derived from or even necessarily related to the parts of the cloning vectors. Likewise the cloning vectors typically will contain the parts necessary for acting as a shuttle vector, in any of the ways discussed herein. However, the

- 5 cloning vectors can also be designed to function only in yeast, for example, and then later retrofitted if desired to function in other systems.

a) Size

The size of the vector construct can vary from 10 kb to 30 kb. The size of the vector construct if it is to be a shuttle between yeast and mammalian cells would be
10 based on the largest chromosome that can be maintained in the yeast. This is typically around 300 kb. In some embodiments it is less than or equal to about 1 mega base, or 900 kb, or 850 kb, or 800 kb, or 750 kb, or 700 kb, or 650 kb, or 600 kb, or 550 kb, or 500 kb, or 450 kb, or 400 kb, or 350 kb, or 250 kb, or 200 kb, or 150 kb, or 100 kb, or 50 kb.

- 15 When the vector is to be shuttled between a BAC and a YAC or a BAC and a MAC the size typically is controlled by the bacterial requirements. This size is typically less than or equal to about 500 kb, 450 kb, or 400 kb, or 350 kb, or 250 kb, or 200 kb, or 150 kb, or 100 kb, or 50 kb.

b) Content

- 20 The cloning vectors should contain a yeast cassette (i.e. a yeast selectable marker, a yeast origin of replication and a yeast centromere), a bacterial cassette (i.e. E. coli selectable marker, and E. coli origin of replication; colE1 or F-factor) and a mammalian selectable marker. Some additional sequences that simplify manipulation with
25 constructs can be included (such as rare cutting recognition sites, or lox sites) as well as sequences that would be required for proper replication of MAC in mammalian cells. These vectors can also have recombination sequences which are discussed herein.

5

3. Cloning vectors

Construction of a TAR vector for isolation of centromeric regions includes cloning of short specific alphoid DNA sequences (hooks) and a counter-selectable marker SUP11.

The hook sequences of the cloning vectors can be designed for other repeat DNA. The hooks, as discussed herein, are specific for the target sequence for cloning. The key point is that there are numerous repetitive sequences known to those of skill in the art which can be cloned using the disclosed vectors and methods.

It needs to be emphasized that selectivity of cloning is due to the use of a combination of a SUP11 gene and specific host strain (i.e. containing yeast prion (Kochneva-Pervukhova et al. Yeast 18:489-497, 2001). Other counter-selectable markers could be other yeast suppressor t-RNA genes or genes that are toxic for yeast (for example a gene encoding a killer-factor toxin (Suzuki et al. Protein Eng. 13:73-76, 2000.)). These genes could be used in the same way to achieve the same result. The limiting factor is whether the selectable marker, such as Sup11 is capable of overcoming the hurdles related to cloning alphoid DNA and other repetitive DNA sequences.

B. Methods of making the compositions

The TAR method allows for the selective isolation of centromeric regions from any cell line and from any chromosome. In contrast, other methods of isolation of the Y chromosome alphoid DNA can only be applied for a cell line carrying a yeast selectable marker and yeast centromere integrated into a specific region. (Kouprina et al., Genome Research 8: 666-672, 1998).

5

1. TAR

Isolation of specific chromosomal regions and entire genes has typically involved a long and laborious process of identification of the region of interest among thousands random YAC clones. Using the recently developed TAR (Transformation-Associated Recombination) cloning technique in the yeast *Saccharomyces cerevisiae*, it has been possible to directly isolate specific chromosomal regions and genes from complex genomes as large linear or circular YACs (Kouprina and Larionov, Current protocols in Human Genetics 5. 17-1 – 5. 17.21, 1999). The speed and efficiency of TAR cloning, as compared to the more traditional methods of gene isolation, provides a powerful tool for the analysis of gene structure and function. Isolation of specific regions from complex genomes by Transformation-Associated Recombination (TAR) in yeast includes preparation of yeast spheroplasts and transformation of the spheroplasts by gently isolated total genomic DNA along with a TAR vector containing sequences homologous to a region of interest. Recombination between a genomic fragment and the vector results in a rescue of the region as a circular Yeast Artificial Chromosome (YAC. When both 3' and 5' ends sequence information is available, a gene can be isolated by a vector containing two short unique sequences flanking the gene (hooks. If sequence information is available only for one gene end [for example, for the 3' end based on Expressed Sequence Tag (EST) information], the gene can be isolated by a TAR vector that has one unique hook corresponding this end and a repeated sequence as a second hook (*Alu* or *B1* repeats for human or mouse DNA, respectively). Because only one of the ends is fixed, this type of cloning is called radial TAR cloning. TAR cloning produces libraries in which nearly 1% of the transformants contain the desired gene. A clone containing a gene of interest can be easily identified in the libraries by PCR.

5

The disclosed methods utilize the vectors disclosed herein to be able to isolate the aliphoid or repetitive DNA sequences.

C. Methods of using the compositions

1. Delivery of the compositions to cells

10 Three methods were examined for the introduction of the BAC/YACs into mammalian cells: electroporation, lipofection and calcium phosphate precipitation. The compositions can also be delivered through a variety of nucleic acid delivery systems, direct transfer of genetic material, in but not limited to, plasmids, viral vectors, viral nucleic acids, phage nucleic acids, phages, cosmids, or via transfer of
15 genetic material in cells or carriers such as cationic liposomes. Such methods are well known in the art and readily adaptable for with the MACSs described herein. In certain cases, the methods will be modified to specifically function with large DNA molecules. Further, these methods can be used to target certain diseases and cell populations by using the targeting characteristics of the carrier. Transfer vectors can be any nucleotide
20 construction used to deliver genes into cells (e.g., a plasmid), or as part of a general strategy to deliver genes, e.g., as part of recombinant retrovirus or adenovirus (Ram et al. Cancer Res. 53:83-88, (1993)). Appropriate means for transfection, including viral vectors, chemical transfectants, or physico-mechanical methods such as electroporation and direct diffusion of DNA, are described by, for example, Wolff, J. A., et al., Science,
25 247, 1465-1468, (1990); and Wolff, J. A. Nature, 352, 815-818, (1991).

As used herein, plasmid or viral vectors are agents that transport the MAC into the cell without degradation and include a promoter yielding expression of the gene in the cells into which it is delivered. In some embodiments the MACs are derived from either a virus or a retrovirus. Viral vectors are Adenovirus, Adeno-associated virus,

- 5 Herpes virus, Vaccinia virus, Polio virus, AIDS virus, neuronal trophic virus, Sindbis and other RNA viruses, including these viruses with the HIV backbone. Also preferred are any viral families which share the properties of these viruses which make them suitable for use as vectors. Retroviruses include Murine Maloney Leukemia virus, MMLV, and retroviruses that express the desirable properties of MMLV as a vector.
- 10 Retroviral vectors are able to carry a larger genetic payload, i.e., a transgene or marker gene, than other viral vectors, and for this reason are a commonly used vector. However, they are not as useful in non-proliferating cells. Adenovirus vectors are relatively stable and easy to work with, have high titers, and can be delivered in aerosol formulation, and can transfect non-dividing cells. Pox viral vectors are large and have
- 15 several sites for inserting genes, they are thermostable and can be stored at room temperature. A preferred embodiment is a viral vector which has been engineered so as to suppress the immune response of the host organism, elicited by the viral antigens. Preferred vectors of this type will carry coding regions for Interleukin 8 or 10.

- Viral vectors can have higher transaction (ability to introduce genes) abilities
- 20 than chemical or physical methods to introduce genes into cells. Typically, viral vectors contain, nonstructural early genes, structural late genes, an RNA polymerase III transcript, inverted terminal repeats necessary for replication and encapsidation, and promoters to control the transcription and replication of the viral genome. When engineered as vectors, viruses typically have one or more of the early genes removed
- 25 and a gene or gene/promotor cassette is inserted into the viral genome in place of the removed viral DNA. Constructs of this type can carry up to about 8 kb of foreign genetic material. The necessary functions of the removed early genes are typically supplied by cell lines which have been engineered to express the gene products of the early genes in trans.

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a) Retroviral Vectors

A retrovirus is an animal virus belonging to the virus family of Retroviridae, including any types, subfamilies, genus, or tropisms. Retroviral vectors, in general, are described by Verma, I.M., Retroviral vectors for gene transfer. In Microbiology-1985, 10 American Society for Microbiology, pp. 229-232, Washington, (1985), which is incorporated by reference herein. Examples of methods for using retroviral vectors for gene therapy are described in U.S. Patent Nos. 4,868,116 and 4,980,286; PCT applications WO 90/02806 and WO 89/07136; and Mulligan, (Science 260:926-932 (1993)); the teachings of which are incorporated herein by reference.

15 A retrovirus is essentially a package which has packed into it nucleic acid cargo. The nucleic acid cargo carries with it a packaging signal, which ensures that the replicated daughter molecules will be efficiently packaged within the package coat. In addition to the package signal, there are a number of molecules which are needed in cis, for the replication, and packaging of the replicated virus. Typically a retroviral 20 genome, contains the gag, pol, and env genes which are involved in the making of the protein coat. It is the gag, pol, and env genes which are typically replaced by the foreign DNA that it is to be transferred to the target cell. Retrovirus vectors typically contain a packaging signal for incorporation into the package coat, a sequence which signals the start of the gag transcription unit, elements necessary for reverse 25 transcription, including a primer binding site to bind the tRNA primer of reverse transcription, terminal repeat sequences that guide the switch of RNA strands during DNA synthesis, a purine rich sequence 5' to the 3' LTR that serve as the priming site for the synthesis of the second strand of DNA synthesis, and specific sequences near the ends of the LTRs that enable the insertion of the DNA state of the retrovirus to insert 30 into the host genome. The removal of the gag, pol, and env genes allows for about 8 kb of foreign sequence to be inserted into the viral genome, become reverse transcribed ,

5 and upon replication be packaged into a new retroviral particle. This amount of nucleic acid is sufficient for the delivery of a one to many genes depending on the size of each transcript. It is preferable to include either positive or negative selectable markers along with other genes in the insert.

Since the replication machinery and packaging proteins in most retroviral
10 vectors have been removed (gag, pol, and env), the vectors are typically generated by placing them into a packaging cell line. A packaging cell line is a cell line which has been transfected or transformed with a retrovirus that contains the replication and packaging machinery, but lacks any packaging signal. When the vector carrying the DNA of choice is transfected into these cell lines, the vector containing the gene of
15 interest is replicated and packaged into new retroviral particles, by the machinery provided in cis by the helper cell. The genomes for the machinery are not packaged because they lack the necessary signals.

b) Adenoviral Vectors

The construction of replication-defective adenoviruses has been described
20 (Berkner et al., J. Virology 61:1213-1220 (1987); Massie et al., Mol. Cell. Biol. 6:2872-2883 (1986); Haj-Ahmad et al., J. Virology 57:267-274 (1986); Davidson et al., J. Virology 61:1226-1239 (1987); Zhang "Generation and identification of recombinant adenovirus by liposome-mediated transfection and PCR analysis" BioTechniques 15:868-872 (1993)). The benefit of the use of these viruses as vectors
25 is that they are limited in the extent to which they can spread to other cell types, since they can replicate within an initial infected cell, but are unable to form new infectious viral particles. Recombinant adenoviruses have been shown to achieve high efficiency gene transfer after direct, in vivo delivery to airway epithelium, hepatocytes, vascular endothelium, CNS parenchyma and a number of other tissue sites (Morsy, J. Clin.
30 Invest. 92:1580-1586 (1993); Kirshenbaum, J. Clin. Invest. 92:381-387 (1993); Roessler, J. Clin. Invest. 92:1085-1092 (1993); Moullier, Nature Genetics 4:154-159

- 5 (1993); La Salle, *Science* 259:988-990 (1993); Gomez-Foix, *J. Biol. Chem.* 267:25129-25134 (1992); Rich, *Human Gene Therapy* 4:461-476 (1993); Zabner, *Nature Genetics* 6:75-83 (1994); Guzman, *Circulation Research* 73:1201-1207 (1993); Bout, *Human Gene Therapy* 5:3-10 (1994); Zabner, *Cell* 75:207-216 (1993); Caillaud, *Eur. J. Neuroscience* 5:1287-1291 (1993); and Ragot, *J. Gen. Virology* 74:501-507
- 10 (1993)). Recombinant adenoviruses achieve gene transduction by binding to specific cell surface receptors, after which the virus is internalized by receptor-mediated endocytosis, in the same manner as wild type or replication-defective adenovirus (Chardonnet and Dales, *Virology* 40:462-477 (1970); Brown and Burlingham, *J. Virology* 12:386-396 (1973); Svensson and Persson, *J. Virology* 55:442-449 (1985);
- 15 Seth, et al., *J. Virol.* 51:650-655 (1984); Seth, et al., *Mol. Cell. Biol.* 4:1528-1533 (1984); Varga et al., *J. Virology* 65:6061-6070 (1991); Wickham et al., *Cell* 73:309-319 (1993)).

A viral vector can be one based on an adenovirus which has had the E1 gene removed and these virions are generated in a cell line such as the human 293 cell line.

- 20 In another preferred embodiment both the E1 and E3 genes are removed from the adenovirus genome.

Another type of viral vector is based on an adeno-associated virus (AAV). This defective parvovirus is a preferred vector because it can infect many cell types and is nonpathogenic to humans. AAV type vectors can transport about 4 to 5 kb and wild

25 type AAV is known to stably insert into chromosome 19. Vectors which contain this site specific integration property are preferred. An especially preferred embodiment of this type of vector is the P4.1 C vector produced by Avigen, San Francisco, CA, which can contain the herpes simplex virus thymidine kinase gene, HSV-tk, and/or a marker gene, such as the gene encoding the green fluorescent protein, GFP.

- 30 The inserted genes in viral and retroviral usually contain promoters, and/or enhancers to help control the expression of the desired gene product. A promoter is generally a sequence or sequences of DNA that function when in a relatively fixed

- 5 location in regard to the transcription start site. A promoter contains core elements required for basic interaction of RNA polymerase and transcription factors, and may contain upstream elements and response elements.

c) Large payload viral vectors

10 Molecular genetic experiments with large human herpesviruses have provided a means whereby large heterologous DNA fragments can be cloned, propagated and established in cells permissive for infection with herpesviruses (Sun et al., Nature genetics 8: 33-41, 1994; Cotter and Robertson, Curr Opin Mol Ther 5: 633-644, 1999). These large DNA viruses (herpes simplex virus (HSV) and Epstein-Barr virus (EBV), have the potential to deliver fragments of human heterologous DNA > 150 kb to
15 specific cells. EBV recombinants can maintain large pieces of DNA in the infected B-cells as episomal DNA. Individual clones carried human genomic inserts up to 330 kb appeared genetically stable. The maintenance of these episomes requires a specific EBV nuclear protein, EBNA1, constitutively expressed during infection with EBV. Additionally, these vectors can be used for transfection, where large amounts of protein
20 can be generated transiently in vitro. Herpesvirus amplicon systems are also being used to package pieces of DNA > 220 kb and to infect cells that can stably maintain DNA as episomes. Other cloning systems based on mammalian viruses are also can be combined with MAC system. For example, replicating and host-restricted non-replicating vaccinia virus vectors.

25 The disclosed compositions can be delivered to the target cells in a variety of ways. For example, the compositions can be delivered through electroporation, or through lipofection, or through calcium phosphate precipitation. The delivery mechanism chosen will depend in part on the type of cell targeted and whether the delivery is occurring for example in vivo or in vitro. For example, a preferred mode of
30 delivery for in vivo uses would be the use of liposomes. Lipofection has yielded ~5 x

5 10^{-5} neomycin-resistant transfectants per microgram of BAC/YAC DNA. The efficiency was much lower using the other procedures.

Thus, the compositions can comprise, in addition to the disclosed MACs or vectors for example, lipids such as liposomes, such as cationic liposomes (e.g., DOTMA, DOPE, DC-cholesterol) or anionic liposomes. Liposomes can further
10 comprise proteins to facilitate targeting a particular cell, if desired. Administration of a composition comprising a compound and a cationic liposome can be administered to the blood afferent to a target organ or inhaled into the respiratory tract to target cells of the respiratory tract. Regarding liposomes, see, e.g., Brigham et al. *Am. J. Resp. Cell. Mol. Biol.* 1:95-100 (1989); Felgner et al. *Proc. Natl. Acad. Sci USA* 84:7413-7417
15 (1987); U.S. Pat. No.4,897,355. Furthermore, the compound can be administered as a component of a microcapsule that can be targeted to specific cell types, such as macrophages, or where the diffusion of the compound or delivery of the compound from the microcapsule is designed for a specific rate or dosage.

As described above, the compositions can be administered in a
20 pharmaceutically acceptable carrier and can be delivered to the subject's cells *in vivo* and/or *ex vivo* by a variety of mechanisms well known in the art (e.g., uptake of naked DNA, liposome fusion, intramuscular injection of DNA via a gene gun, endocytosis and the like).

If *ex vivo* methods are employed, cells or tissues can be removed and
25 maintained outside the body according to standard protocols well known in the art. The compositions can be introduced into the cells via any gene transfer mechanism, such as, for example, calcium phosphate mediated gene delivery, electroporation, microinjection or proteoliposomes. The transduced cells can then be infused (e.g., in a pharmaceutically acceptable carrier) or homotopically transplanted back into the
30 subject per standard methods for the cell or tissue type. Standard methods are known for transplantation or infusion of various cells into a subject.

5 In the methods described above which include the administration and uptake of
exogenous DNA into the cells of a subject (i.e., gene transduction or transfection),
delivery of the compositions to cells can be via a variety of mechanisms. As one
example, delivery can be via a liposome, using commercially available liposome
preparations such as LIPOFECTIN, LIPOFECTAMINE (GIBCO-BRL, Inc.,
10 Gaithersburg, MD), SUPERFECT (Qiagen, Inc. Hilden, Germany) and
TRANSFECTAM (Promega Biotec, Inc., Madison, WI), as well as other liposomes
developed according to procedures standard in the art. In addition, the nucleic acid or
vector of this invention can be delivered *in vivo* by electroporation, the technology for
which is available from Genetronics, Inc. (San Diego, CA) as well as by means of a
15 SONOPORATION machine (ImaRx Pharmaceutical Corp., Tucson, AZ).

2. Delivery of pharmaceutical products

As described above, the compositions can also be administered *in vivo* in a
pharmaceutically acceptable carrier. By "pharmaceutically acceptable" is meant a
material that is not biologically or otherwise undesirable, i.e., the material may be
20 administered to a subject, along with the nucleic acid or vector, without causing any
undesirable biological effects or interacting in a deleterious manner with any of the
other components of the pharmaceutical composition in which it is contained. The
carrier would naturally be selected to minimize any degradation of the active ingredient
and to minimize any adverse side effects in the subject, as would be well known to one
25 of skill in the art.

The compositions may be administered orally, parenterally (e.g., intravenously),
by intramuscular injection, by intraperitoneal injection, transdermally, extracorporeally,
topically or the like, although topical intranasal administration or administration by
inhalant is typically preferred. As used herein, "topical intranasal administration"
30 means delivery of the compositions into the nose and nasal passages through one or
both of the nares and can comprise delivery by a spraying mechanism or droplet

5 mechanism, or through aerosolization of the nucleic acid or vector. The latter may be effective when a large number of animals is to be treated simultaneously.

Administration of the compositions by inhalant can be through the nose or mouth via delivery by a spraying or droplet mechanism. Delivery can also be directly to any area of the respiratory system (e.g., lungs) via intubation. The exact amount of the

10 compositions required will vary from subject to subject, depending on the species, age, weight and general condition of the subject, the severity of the allergic disorder being treated, the particular nucleic acid or vector used, its mode of administration and the like. Thus, it is not possible to specify an exact amount for every composition.

However, an appropriate amount can be determined by one of ordinary skill in the art

15 using only routine experimentation given the teachings herein.

Parenteral administration of the composition, if used, is generally characterized by injection. Injectables can be prepared in conventional forms, either as liquid solutions or suspensions, solid forms suitable for solution or suspension in liquid prior to injection, or as emulsions. A more recently revised approach for parenteral

20 administration involves use of a slow release or sustained release system such that a constant dosage is maintained. See, e.g., U.S. Patent No. 3,610,795, which is incorporated by reference herein.

The materials may be in solution, suspension (for example, incorporated into microparticles, liposomes, or cells). These may be targeted to a particular cell type via

25 antibodies, receptors, or receptor ligands. The following references are examples of the use of this technology to target specific proteins to tumor tissue (Senter, et al., Bioconjugate Chem., 2:447-451, (1991); Bagshawe, K.D., Br. J. Cancer, 60:275-281, (1989); Bagshawe, et al., Br. J. Cancer, 58:700-703, (1988); Senter, et al., Bioconjugate Chem., 4:3-9, (1993); Battelli, et al., Cancer Immunol. Immunother., 35:421-425, (1992); Pietersz and McKenzie, Immunolog. Reviews, 129:57-80, (1992); and Roffler, et al., Biochem. Pharmacol., 42:2062-2065, (1991)). Vehicles such as "stealth" and other antibody conjugated liposomes (including lipid mediated drug targeting to

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5 colonic carcinoma), receptor mediated targeting of DNA through cell specific ligands, lymphocyte directed tumor targeting, and highly specific therapeutic retroviral targeting of murine glioma cells *in vivo*. The following references are examples of the use of this technology to target specific proteins to tumor tissue (Hughes et al., Cancer Research, 49:6214-6220, (1989); and Litzinger and Huang, Biochimica et Biophysica Acta, 1104:179-187, (1992)). In general, receptors are involved in pathways of endocytosis, either constitutive or ligand induced. These receptors cluster in clathrin-coated pits, enter the cell via clathrin-coated vesicles, pass through an acidified endosome in which the receptors are sorted, and then either recycle to the cell surface, become stored intracellularly, or are degraded in lysosomes. The internalization pathways serve a variety of functions, such as nutrient uptake, removal of activated proteins, clearance of macromolecules, opportunistic entry of viruses and toxins, dissociation and degradation of ligand, and receptor-level regulation. Many receptors follow more than one intracellular pathway, depending on the cell type, receptor concentration, type of ligand, ligand valency, and ligand concentration. Molecular and cellular mechanisms of receptor-mediated endocytosis has been reviewed (Brown and Greene, DNA and Cell Biology 10:6, 399-409 (1991)).

a) Pharmaceutically Acceptable Carriers

The compositions, including antibodies, can be used therapeutically in combination with a pharmaceutically acceptable carrier.

25 Pharmaceutical carriers are known to those skilled in the art. These most typically would be standard carriers for administration of drugs to humans, including solutions such as sterile water, saline, and buffered solutions at physiological pH. The compositions can be administered intramuscularly or subcutaneously. Other compounds will be administered according to standard procedures used by those skilled in the art.

30

5 Pharmaceutical compositions may include carriers, thickeners, diluents, buffers, preservatives, surface active agents and the like in addition to the molecule of choice. Pharmaceutical compositions may also include one or more active ingredients such as antimicrobial agents, antiinflammatory agents, anesthetics, and the like.

 The pharmaceutical composition may be administered in a number of ways
10 depending on whether local or systemic treatment is desired, and on the area to be treated. Administration may be topically (including ophthalmically, vaginally, rectally, intranasally), orally, by inhalation, or parenterally, for example by intravenous drip, subcutaneous, intraperitoneal or intramuscular injection. The disclosed antibodies can be administered intravenously, intraperitoneally, intramuscularly, subcutaneously,
15 intracavity, or transdermally.

 Preparations for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Aqueous carriers include water, alcoholic/aqueous
20 solutions, emulsions or suspensions, including saline and buffered media. Parenteral vehicles include sodium chloride solution, Ringer's dextrose, dextrose and sodium chloride, lactated Ringer's, or fixed oils. Intravenous vehicles include fluid and nutrient replenishers, electrolyte replenishers (such as those based on Ringer's dextrose), and the like. Preservatives and other additives may also be present such as, for example,
25 antimicrobials, anti-oxidants, chelating agents, and inert gases and the like.

 Formulations for topical administration may include ointments, lotions, creams, gels, drops, suppositories, sprays, liquids and powders. Conventional pharmaceutical carriers, aqueous, powder or oily bases, thickeners and the like may be necessary or desirable.

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5 Compositions for oral administration include powders or granules, suspensions or solutions in water or non-aqueous media, capsules, sachets, or tablets. Thickeners, flavorings, diluents, emulsifiers, dispersing aids or binders may be desirable.

 Some of the compositions may potentially be administered as a pharmaceutically acceptable acid- or base- addition salt, formed by reaction with
10 inorganic acids such as hydrochloric acid, hydrobromic acid, perchloric acid, nitric acid, thiocyanic acid, sulfuric acid, and phosphoric acid, and organic acids such as formic acid, acetic acid, propionic acid, glycolic acid, lactic acid, pyruvic acid, oxalic acid, malonic acid, succinic acid, maleic acid, and fumaric acid, or by reaction with an inorganic base such as sodium hydroxide, ammonium hydroxide, potassium hydroxide,
15 and organic bases such as mono-, di-, trialkyl and aryl amines and substituted ethanolamines.

b) Therapeutic Uses

 The dosage ranges for the administration of the compositions are those large enough to produce the desired effect in which the symptoms disorder are effected. The
20 dosage should not be so large as to cause adverse side effects, such as unwanted cross-reactions, anaphylactic reactions, and the like. Generally, the dosage will vary with the age, condition, sex and extent of the disease in the patient and can be determined by one of skill in the art. The dosage can be adjusted by the individual physician in the event of any counterindications. Dosage can vary, and can be administered in one or
25 more dose administrations daily, for one or several days.

 Other MACs which do not have a specific pharmaceutical function, but which may be used for tracking changes within cellular chromosomes or for the delivery of diagnostic tools for example can be delivered in ways similar to those described for the pharmaceutical products.

30

5 The cloning vectors can used for example as tools to isolate and study target sequences necessary for the completion of the Human Genome project. Repetitive DNA is very difficult to clone, and the methods and reagents disclosed herein have made it possible to clone these types of sequences, for example alphoid sequence or alpha satellite sequence.

10 The MACs can also be used for example as tools to isolate and test new drug candidates for a variety of diseases. They can also be used for the continued isolation and study, for example, the cell cycle. Their use as exogenous DNA delivery devices can be expanded for nearly any reason desired by those of skill in the art.

D. Examples

15 The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how the compounds, compositions, articles, devices and/or methods claimed herein are made and evaluated, and are intended to be purely exemplary of the invention and are not intended to limit the scope of what the inventors regard as their invention. Efforts have been made to
20 ensure accuracy with respect to numbers (e.g., amounts, temperature, etc.), but some errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, temperature is in °C or is at ambient temperature, and pressure is at or near atmospheric.

25 1. Example 1 TAR isolation of Y chromosome derived alphoid DNA

a) Materials and Methods

(1) Yeast Strain and Transformation

The highly transformable *Saccharomyces cerevisiae* strain VL6-48 (MAT alpha,

5 his3- Δ 1, trp1- Δ 1, ura3-52, lys2, ade2-101, met14 cir⁰) (Kouprina and Larionov, ,*Current Protocols in Human Genetics* 1: 5.17.1-5.17.21 (1999)) was used for transformations. Spheroplasts that enable efficient transformation were prepared by using a previously described protocol (Kouprina and Larionov, ,*Current Protocols in Human Genetics* 1: 5.17.1-5.17.21 (1999). For transformation experiments, the DNA-
10 containing plugs (25 μ l, containing about 5 μ g of genomic DNA were melted and treated with agarase. Yeast transformants were selected on synthetic complete medium plates lacking uracil.

(2) TAR cloning of alphoid DNA arrays

The vector used for cloning alphoid DNA from the Y chromosome was vector
15 similar to the vector disclosed in Example 3. The method used for the TAR cloning was similar to the method disclosed in Example 2 and elsewhere. This vector is sufficient to clone many centromeric regions from a variety of different chromosomes, as exemplified by the multiple different centromere regions disclosed herein which were cloned with this vector.

20 (3) Preparation of Chromosomal-sized DNA in Solid Agarose Plugs for the Rescue Transformation Experiments

For isolation of the chromosome Y centromeric region, agarose plugs
containing a high molecular weight genomic DNA were prepared from normal human
25 leukocytes or from Δ Yp74 hybrid cells. The Δ Yp74 hybrid (rodent-human) cell line containing the truncated human chromosome Y was kindly provided by Dr. William Brown (Oxford University, Heller et al., Proc. Natl. Acad. Sci. USA 93: 7125-7130, 1996). About 4×10^9 cells from the Δ Yp74 hybrid cell line carrying a 12 Mb human mini-chromosome (Heller et al., 1996) were pelleted and resuspended in 3.0 ml of TE
30 (50 mM EDTA, 10 mM Tris, pH 7.5). This cell mix was separated in 500 μ l aliquots and placed at 42°C. An equal volume of pre-warmed 1% agarose/EDTA (low-melting

5 agarose in 125 mM EDTA, pH 7.5) were added to each aliquot, mixed completely by vortexing and poured into Bio-Rad molds. Agarose plugs (75 μ l) containing approximately 15 μ g of high molecular weight DNA were prepared using a standard procedure (Kouprina and Larionov, *Current Protocols in Human Genetics* 1: 5.17.1-5.17.21 (1999).

10 (4) Characterization of YAC Clones

Chromosome size DNAs from yeast transformants carrying circular or linear YACs were separated by CHEF, blotted and hybridized with either a 5.7 kb alphoid probe which specifically hybridizes with the centromere of the chromosome Y or a Neo-specific probe. To estimate the size of circular YACs, agarose DNA plugs
15 prepared from yeast transformants were exposed to a low dose of gamma-rays (5 krad) before TAFE analysis. At this dose approximately 10% of 100-200 kb circular DNA molecules are linearized (Larionov et al., *proc. Natl. Acad. Sci. USA* 93: 13925-13930, 1996).

(5) Labeling of DNA Probes

20 A 5.7 kb alphoid DNA fragment was labeled by nick-translation. A Neo-specific probe was labeled by PCR using a 300 bp fragment as a template. The fragment itself was amplified with a pair of primers developed for ORF of the Neo gene. By a similar way URA3 and HIS3 probes were prepared.

(6) Southern Blot Analysis

25 Southern blot hybridization was performed by utilizing 32 P labeled probes and the protocol described by Church and Gilbert (*Proc. Natl. Acad. Sci. USA* 7: 1991-1995, 1984). The membrane blots were incubated for 2 hrs at 65°C in a pre-hybridization solution: 0.5 M Na-phosphate buffer containing 7% SDS and 100 μ g/ml salmon DNA. 20 μ l of a labeled probe was heat denatured in a boiling water for 5

5 minutes and then snap cooled on ice. The Neo probe was added to the hybridization buffer and allowed to hybridize overnight at 65°C. The alphoid probe allowed to hybridize overnight at 78°C (Oakey and Tyler-Smith, Genomics 7: 325-330,1990). The hybridization solution was removed from blots and the blots were washed twice in 2xSSC (1xSSC is 150 mM NaCl and 15 mM sodium citrate, pH 7.0), 0.1% SDS for 30 min at room temperature. Then the blots were washed three times in 0.1xSSC, 0.1% SDS for 30 min at 65°C. Blots were exposed to X-ray film for 24-72 h at -70°C.

(7) Fluorescent in situ Hybridization (FISH)

To analyze alphoid DNA in HT1080 transfectants, 500 ng of a 5.7 kb alphoid DNA repeat from the Y chromosome was labeled with bio-11-dUTP using the Gibco BRL Nick Translation System. A mixture of 200 ng of biotinylated DNA and 30 µg of human CotI DNA (BRL) was hybridized to metaphase chromosomes in a volume of 27 µl under a cover slip (22 x22 mm) as previously described with minor modification (McCormick et al 1993). After hybridization at 37°C for about 19 h, slides were washed and stained using fluorescent avidin and counterstained with propidium iodide.

20 (8) Construction of the vector pRS-Sat-Neo for circularization of linear YACs

The circularizing vector pRS-Sat-Neo was constructed as follows. First, the Neo fragment was amplified as a 2.7 kb fragment by PCR using a pair of primers containing overhanging NotI and XhoI sequences, in addition to the Neo site. PCR was performed using a BRV1 plasmid (Kouprina et al., Proc. Natl. Acad. Sci. U.S.A. 95; 4469-4474,1998) as a template. The matched set of primers were: Neo Not Rev (5'-gcggatgaatggcagaaattcgat-3') (SEQ ID NO:49) and Neo Xho For (5'-ccggctcgagctgtggaatgtgtgtcagtagg-3') (SEQ ID NO:50). Then a 1.0 kb XmaI-BglII fragment was excised from the 2.7 kb Neo PCR product and cloned into SmaI-BamH sites of pRS313 (ARS-CEN6-HIS3-AmpR) (Sikorski and Hieter, Genetics 122: 19-27, 1989). The 1.0 kb fragment contains the Neo gene open reading frame but does not

5 contain the SV40 promoter. Then a 110 bp alpha-satellite fragment was amplified by PCR using primers containing SalI sequences in addition to the satellite-specific primers. PCR was performed using human genomic DNA (Promega) as a template. The matched set of primers were: Sat Sal Rev (5'-ACCGTCGACTCACAGAGTTGAA-3' SEQ ID NO:47) and Sat Sal For (5'-ATTCCCGTTTCCAACGAAGG-3' SEQ ID NO:48). Total length of the amplified alpha-satellite fragment was 117 bp. This alpha-satellite fragment was cloned into pCRII plasmid (Invitrogen), then isolated as an EcoRI fragment and cloned into a EcoRI site of pRS-Neo. The constructed vector pRS-Sat-Neo was cut with SmaI (the site is located between the targeting sequences) before transformation to yield linear molecules bounded by the Sat and Neo hooks. Plasmid DNA isolation was performed using a Qiagen Plasmid Purification Kit. The standard lithium acetate procedure) was used for YAC circularization. Yeast transformants were selected on synthetic complete medium plates lacking histidine.

20 (9) Retrofitting of circular YACs into BACs for Propagation in Bacterial and Mammalian Cells

Retrofitting of circular YACs into BACs was accomplished through the use of a yeast-bacteria-mammalian cell shuttle vector, BRV1, containing the F-factor origin of replication and the Neo^R gene (Kouprina et al, Proc. Natl. Acad. Sci USA 95: 4469-4474, 1998), by a standard lithium acetate transformation procedure. Yeast transformants were selected on synthetic complete medium plates lacking uracil. The retrofitted His⁺Ura⁺ YACs were moved to *E. coli* by electroporation.

(10) Transfer of YAC/BACs into *E. coli* cells

Low-melting-point agarose plugs were prepared from yeast His⁺Ura⁺ transformants using a standard method (Kouprina and Larionov, *Current Protocols in Human Genetics* 1: 5.17.1-5.17.21 (1999)). One microliter of the melted and treated plug was electroporated into 20 µl of the *E. coli* DH10B competent cells (Gibco BRL) using a Bio-Rad Gene Pulser with the

5

settings at 2.5 kV, 200 ohms and 25 μ F. Colonies were selected on LB plates containing chloramphenicol at a concentration of 12.5 μ g/ml.

(11) Restriction Analysis of BACs

BACs were isolated from *E.coli* utilizing a Qiagen Plasmid Purification kit (Cat. # 12163, Qiagen Inc., Santa Clarita, CA). Restriction analysis was performed on BAC DNAs as follows. To estimate size of inserts, 5 μ l of BAC DNA was digested with 0.1 U NotI restriction enzyme (New England Biolabs). The digestion was analyzed by CHEF (Clamped Homogeneous Electrical Field). To analyse the organization of the alphoid DNA inserts in BACs, 5 μ l of BAC DNA was digested either with EcoRI, XbaI, SpeI or double digested with EcoRI and SpeI. Samples were loaded onto a 1.2% agarose gel in 1x TBE (0.09M Tris-borate, 0.002M EDTA).

(12) DNA sequencing

5.7 kb EcoRI, 2.8 kb SpeI, 2.9 kb SpeI and 1.6 kb SpeI fragments containing blocks of satellite repeats were gel purified after a 250 kb BAC DNA digestion and cloned into either EcoRI or SpeI sites of the pRS313 plasmid (Sikorski and Hieter, 1989) for further sequencing analysis. DNA sequencing was performed using T3 and T7 primers and a Rhodamine Dye Terminator Cycle Sequencing Kit (Perkin Elmer, Catalog No 403 042) in conjunction with an automated DNA sequencer, Model 377 (Perkin Elmer).

b) Results

To isolate an alphoid DNA array from a functional centromere, we used normal human leukocytes and Δ Yq74 hybrid cell line containing a fragment of the Y human mini-chromosome (Brown et al., Hum. Mol. Genet. 3: 1227-1237, 1994; Heller et al.,

5 Proc. Natl. Acad. Sci. USA 93: 7125-7130,1996). This mini-chromosome was generated by two rounds of telomere-directed chromosome breakage (Barnett et al., Nucleic Acids Res. 21: 27-36,1993). One of the breakages that occurred within the centromeric array of alphoid satellite DNA deleted the entire long arm of the chromosome and thus generated a short arm acrocentric derivative, $\Delta Yq74$, composed of only 140 kb of alphoid DNA and the breakage construct. The resulting mini-chromosome was linear and sized at approximately 12 Mb. Cytogenetic analysis indicated that the mini-chromosome was stably maintained by cells proliferating in culture for about 100 cell divisions in the absence of any applied selection and segregated accurately at mitotic anaphase (Heller et al., Proc. Natl. Acad. Sci. USA 93: 15 7125-7130,1996). This result suggested that 140 kb of alphoid DNA is sufficient for accurate chromosome segregation but that other sequences may be required for full centromere function.

The strategy of isolation of the alphoid DNA arrays from the $\Delta Yq74$ hybrid cell line is based on our observation that a targeted chromosomal region can be rescued as a YAC by yeast transformation (Kouprina et al., Genome Research 8: 666-672, 1998). The truncation of the chromosome Y was done with the vector containing a human telomere, 5.7 kb of chromosome Y alphoid unit, the neomycin gene and a yeast cassette consisting of the URA3 selectable marker, an origin of replication and a centromere. Previously we have demonstrated that the targeted chromosomal region containing the minimum requirements for its propagation in yeast cells (CEN, ARS and a selectable marker) can be rescued as a YAC simply by transformation of the total genomic DNA into yeast spheroplasts and following selection for the marker. We proposed that selection for the URA3 marker present within the 12 Mb mini-chromosome would result in isolation of the chromosome region(s) containing a 140 kb block of alphoid DNA plus a flanking region in the form of linear or circular YACs. Two different scenarios for the rescue of this targeted region may be considered. The presence of multiple (TG)_n telomere-like sequences that are frequent in human DNA (approximately once per 40 kb) and human telomere at the end of the mini-

5 chromosome would provide an opportunity for circularization through homologous recombination and lead to generation of circular YACs. Alternatively, healing of only one broken end of the rescued chromosome fragment(s) in yeast by yeast-like telomeric repeats would lead to establishment of linear YACs. After transformation of yeast spheroplasts by genomic DNA isolated from the hybrid cell line $\Delta Yq74$ and following
10 selection for the URA3 marker, we obtained a set of linear YACs of different size from 100 kb to 250 kb that suggested the second mechanism of rescue of the targeted region.

The alphoid DNA array from a normal Y chromosome has been isolated by a disclosed TAR cloning system that allows the cloning of genomic regions containing only monotonic repeats. This method utilizes a disclosed TAR vector that includes a
15 yeast selectable marker (HIS3), a yeast centromere sequence (CEN6), a yeast origin of replication (ARSH4) and alphoid DNAs as targeting sequences. To eliminate a plasmid background during TAR cloning, a counter-selectable marker (SUP11) was incorporated between the alphoid DNA targeting sequences. Co-transformation of the vector and genomic DNA isolated from normal human leukocytes resulted in rescue of
20 alphoid DNA arrays as circular 50- 250 kb YACs. Approximately 7% of YACs contained alphoid DNA from the Y chromosomes.

To prove that the rescued YACs originated from the centromere of chromosome Y, we have used fluorescence in situ hybridization which provides a quick and direct method for localization of the YACs. Three YACs, 100 kb, 150 kb and 250 kb, chosen
25 for this experiment exhibited one strong signal on the centromere of the chromosome Y under stringent conditions. They are in centromeric region of the Y human chromosome.

c) Retrofitting of YACs into BACs with the mammalian selectable marker

30 BACs have advantages versus YACs because they can be easily purified by

5 alkaline methods for further analysis. Thus, different YAC isolates containing the 100 kb, 170 kb and 250 kb alphoid DNA arrays from the Y chromosome were *retrofitted* by recombination with the vector BRV1 that contained a Neo^R marker and sequences that would enable subsequent propagation as a BAC. These BAC/YACs were then transferred to *E. coli* by electroporation, as described herein. CHEF analysis has shown
10 that the alphoid DNA BACs are quite stable in bacterial cells. Digestion of the BAC DNAs with a NotI restriction enzyme gave one major predicted size band. Fractioning of the deleted BAC forms (visible as minor bands on electrophoregrams) does not exceed 5% in DNA preparations as judged by agarose electrophoresis.

15 d) Characterization of BACs containing blocks of satellite repeats

Tyler-Smith and Brown (1987) have shown that the alphoid DNA within the main block of chromosome Y is organized into tandemly repeating units, most of which are about 5.7 kb long. Each unit consists of 34 tandemly repeated about 170 bp monomers of alphoid DNA and contains a single EcoRI site (Tyler-Smith and Brown,
20 J. Mol. Biol. 195: 457-470,1987). We have shown that indeed alphoid DNA arrays from the Y chromosome consists of two units that can be identified by Spe I digestion (see below). The BACs were digested with either EcoRI or SpeI and analyzed by gel electrophoresis and blot hybridization using alphoid DNA as a probe. The analysis has shown that inserts in 100 kb, 170 kb and 250 kb BACs contained exclusively alphoid
25 DNA. EcoRI digestions generated a main 5.7 kb fragment corresponding to alphoid DNA unit. Intensity of other fragments corresponding to a vector and junction between a vector and an insert was much less. Similar results were obtained with SpeI BAC digestions. Isolation of the 250 kb alphoid DNA array which is bigger than that in the ΔYq74 suggests that this clone arose as a result of rearrangement of original material
30 during isolation in yeast. Taking into account the number of repeats in a centromeric region, the smaller size rescued alphoid DNA arrays could also be rearranged.

5 During restriction analyses of the BACs we found that the alphoid 5.7 kb DNA unit contains two SpeI recognition sites. Digestion of the BACs by SpeI produced two fragments with size 2.8 kb and 2.9 kb. Because SpeI is a rare cutter enzyme, we supposed that SpeI digestion could be used to detect the chromosome Y-specific alphoid sequences in genomic DNAs. Indeed, we observed the 2.8 kb and 2.9 kb fragments
10 seen on electrophoregrams of the SpeI digests of male genomic DNA. The complete sequence of a 5.7 kb alphoid DNA unit was not available; we therefore subcloned the SpeI fragments to determine nucleotide sequences of the entire unit. Based on sequence data, the unit consists of highly diverged monomers (Figure 5A). This level of divergency (between 12% and 30% for different monomers) explains why large
15 blocks of the alphoid DNA can be stably propagated both in yeast and *E. coli* hosts.

 SpeI digestion of the BACs has also identified an additional 1.6 kb fragment containing ten alphoid DNA monomers. Sequence analysis has shown that this fragment contains palindromic duplication of alphoid DNA. Because we failed to detect this fragment in a SpeI digest of male genomic DNAs, we suggest that this
20 inverted duplication was generated during chromosome fragmentation.

 To conclude, our data indicate that in general the organization of alphoid DNA arrays in BAC isolates are similar to that in the mini-chromosome $\Delta Yq74$. However, the isolated arrays can differ from the array in $\Delta Yq74$ by the number of alphoid DNA units.

25 e) Transfection of alphoid DNA constructs into human cells

 Three BACs with different sized alphoid DNA arrays (100 kb, 170 kb and 250 kb) were purified as described in Materials and Methods and introduced into HT1080 cells by lipofection. Following transfection, the cells were placed on G418 selection
30 for 14-18 days. Six drug-resistant colonies were then isolated for each BAC construct and analyzed by fluorescent in situ hybridization (FISH) after culturing off selection for

5 60 days using appropriate alpha-satellite and vector probes. In all 18 drug resistant clones screened by this method for identifying novel alpha-satellite containing chromosomal structures were observed. In 12 clones the transfected alpha-satellite DNA was integrated into endogenous human chromosomes. In 6 clones the transfected alpha-satellite DNA was present as a HAC as well as an integrated form on one of
10 endogenous chromosomes. It should be noted that HACs were poorly visible after DAPI staining. Although the fraction of cells containing a HAC was variable between cell lines, HAC number per cell was most frequently one.

CENP-C has been detected only at the active centromere (Silvian and Schwartz, 1995). We therefore assayed for the presence of this protein on HACs generated by
15 aliphoid DNA constructs. Indirect immunofluorescence with CREST antibodies has shown that this protein is co-localized with a HAC.

To examine the size of HACs, genomic DNA from cell lines containing HACs was gently analyzed in agarose block, gamma-rays irradiated or digested by a rare cutting enzyme and analyzed by blot hybridization. Using these methods we failed to
20 resolve any HAC by CHEF. Physical analysis of HACs was complicated by the presence of integrated copies of input DNA in transfectants. We can not exclude also that HACs are heterogeneous in size in cell population as a result of a loss and gain of aliphoid DNA units during replication.

Because the original HAC constructs contain both BAC and YAC cassettes, the
25 autonomously replicating forms of the HAC in human cells may be rescued by *E. coli* and yeast transformation with high efficiency. At the same time the rescue of integrated copies of the input DNA by transformation seems to be unlikely. Linear DNAs exhibit an extremely low transformation efficiency in *E. coli* and in yeast when recombination-deficient host strains are used (Larionov et al., 1994).

30 We decided to investigate organization of HACs by rescuing the HAC sequences by transformation. To identify optimal conditions for the rescue of HACs by

5 transformation, all reconstruction experiments were done with HT1080 genomic DNA mixed with different amounts of the 150 kb alphoid BAC DNA (1, 2 and 10 copies per genome equivalent). These optimal conditions were used in our experiments on recovering HACs from human cells back into yeast and *E. coli*. A RecA bacterial strain DH10B and a RAD52 deficient yeast host strain were used for transformations. DNAs
10 were prepared from five HAC-containing cell lines and from 5 HAC-negative cell lines carrying integrated copies of the input BAC constructs. The cells used for the rescue experiments passed 40 and 80 generations without selection. The DNAs were then transformed directly either to yeast spheroplasts or to *E. coli* cells using electroporation. Table 2 summarizes the results on yeast and *E. coli* transformation by genomic DNA
15 isolated from HT1080 transfectants. As can be seen, both *E. coli* and yeast transformants can be obtained only with DNAs isolated from the cell lines positive for HACs based on FISH. No transformants were obtained with the same amount of DNA from HAC-negative clones. Based on the yield of transformants in reconstruction experiments with a known amount of BAC DNA, HAC-positive clones contained
20 between 1 and 5 copies of autonomous form of the input DNA.

5 Table 2

Rescue of Autonomous Forms of Circular YAC/BACs After 100 Generations in
Human Cells by Yeast Transformation

	100 kb YAC22	150 kb YAC11	250 kb YAC66
	Neo ^R transfectant	Neo ^R transfectant	Neo ^R transfectant
1	+	+	-
2	+	-	-
3	-	-	+
4	-	-	+
5	+	-	-
6	+	+	-

10 Plasmid DNAs were isolated from *E. coli* and yeast transformants and compared with the original BAC constructs. Analysis of 30 isolates for each of the three BAC constructs (100 kb, 150 kb and 250 kb) has shown that all contain a predicted BAC/YAC cassette, the Neo^R gene and the Y chromosome- specific alphoid DNA sequences. The size of the alphoid DNA arrays varied among individual isolates

15 for each BAC construct. For DNA molecules rescued from a 100 kb MAC (e.g., HAC), the size of alphoid DNA array varied from 40 kb to 100 kb (40kb, 50 kb, 65 kb, 70 kb; 85 kb, 90 kb and 100 kb); for DNAs rescued from a 150 kb HAC the size varied from 60 kb to 150 kb (60 kb, 70 kb, 75 kb, 85 kb, 110 kb, 130 kb, and 150 kb). Similarly, the size of BACs rescued from cells containing a 250 HAC varied from 50

20 kb to 250 kb (50 kb, 60 kb, 75 kb, 80 kb, 120 kb, 175 kb, 180 kb, 210 kb, 250 kb) in individual isolates. Because HACs are presumably multimers in human cells (Harrington et al., 1997, Ikeno et al., 1998; Henning et al., 1999; Ebersole et al., 2000) deletions in YAC/BAC isolates have arisen during a transformation procedure. Physical analyses of rescued BAC and YAC clones did not detect any non-alphoid

25 DNA sequences, suggesting that HAC formation took place without an acquisition of the host DNA.

5 Physical analysis of the YAC clones isolated from normal Y chromosome and
its deleted derivative, $\Delta Yq74$, has shown that the alphoid DNA array is not interrupted
by nonhomologous sequences. Based on restriction mapping and sequencing results,
the Y chromosome alphoid DNA array consists of both direct and inverted repeats of a
5.7 kb alphoid DNA unit. Comparison with the original chromosome has shown that
10 inverted repeats identified in $\Delta Yq74$ have arisen during chromosome Y truncation. The
presence of the inverted repeats indicates that the inverted nature of the repeats does not
inhibit MAC function and may represent a means for inhibiting homologous
recombination events that can take place with large arrays of tandem repeats.

 Three different groups demonstrated the formation of HACs in HT1080 cells
15 after transfection of constructs containing ~a 100 kb block of alphoid DNA (Ikeno et
al., *Nature Biotechnol.* 16: 431-439, 1998; Henning et al., *Proc. Natl. Acad. Sci. USA*
96: 592-597, 1999; Ebersole et al., *Hum. Mol. Genet.* 9: 1623-1631, 2000). Both linear
YAC constructs containing telomeric sequences and circular BACs lacking telomeres
were competent in MAC formation. Alphoid DNAs used for these studies were
20 isolated from two human chromosomes (chromosome 17 and 21). The DNAs are
characterized by uniform higher order repeats and frequent boxes, a conserved motif
binding the CENP-B protein (Muro et al., *J. Cell Biol.* 116: 585-596, 1992). No HAC
formation was observed with the construct containing a block of alphoid DNA lacking
CENP-B boxes (Ikeno et al., *Nature Biotechnol.* 16: 431-439, 1998).

25 Our results demonstrate that the presence of a CENP-B binding sites is not
required for de novo formation of kinetohore. BAC/YAC constructs with alphoid DNA
arrays were isolated from chromosome 22 (this study) and from the Y human
chromosome lacking the CENP-B binding sites (Floridia et al., *Chromosoma* 109: 318-
327, 2000). Nevertheless the constructs efficiently produced HACs during transfection
30 into HT1080 cells. The same yield of HACs was observed for constructs containing
250 kb and 100 kb of alphoid DNA, suggesting that the minimal size of alphoid DNA
required for HAC formation could be even less than 100 kb.

5 The MAC/HAC constructs can contain both BAC and YAC cassettes, and those that do we showed that they can rescue HAC sequences from human cells by *E. coli* and yeast transformation. Physical analyses of the rescued BAC and YAC clones did not detect the presence of any non-alphoid DNA sequences, suggesting that HAC formation took place without an acquisition of the host DNA.

10 As has been shown in previous publications, formation of HACs is accompanied by multimerization of transforming DNAs (Harrington et al., Nature genetics 15: 345-355, 1997, Ikeno et al., Nature Biotechnol. 16: 431-439, 1998; Hcnning et al., Proc. Natl. Acad. Sci. USA 96: 592-597, 1999; Ebersole et al., Hum. Mol. Genet, 9: 1623-1631, 2000). Based on indirect measuring, the size of HACs in
15 transfected cells varied between 2 Mb and 10 Mb. We failed to determine the size of HACs generated by the Y chromosome alphoid DNA array by separation of genomic DNA by CHEF followed blot-hybridization. The most reasonable explanation of that is a heterogeneity in HAC size in cell population. While we did not estimate the HAC size by a direct method, the following observations suggest that the HACs generated
20 from the Y chromosome are maintained in human cells without a significant amplification. 1) The HACs generated by these constructs were poor visible on metaphase plates after DAPI staining. 2) Based on quantitative hybridization, vector-specific sequences, NeoR, URA3 and HIS3 are present in HAC-positive cell lines in 3-8 copies per genome. Because these lines also contain 1-2 integrated copies of the
25 input BAC DNA, there should be no significant amplification of sequences in HAC. 3) The original input DNAs can be rescued from HAC-positive transfectants as BACs or YACs. It is known that megabase-size DNAs do not transform *E. coli* cells.

Additional experiments are required to confirm that in contrast to alphoid DNA arrays from chromosome 17 and 21, the Y chromosome alphoid DNA array generates HACs
30 with a lower level of amplification of the input DNA.

Stable propagation of HACs in HT1080 cells suggests that the HACs not only segregate properly during cell divisions but also replicate in S-phase. It is unlikely that

5 vector sequences (i.e. YAC and BAC cassettes) initiate DNA replication. Since no
exogenous non-alphoid mammalian genomic DNA is contained in the YAC, it is more
likely that DNA replication is initiated within the block of alphoid DNA. If this is a
true, each alphoid DNA unit has a chance to initiate DNA replication similar to that
observed for block of rDNA genes (Kouprina and Larionov, Current genetics 7: 433-
10 438, 1983). This suggestion could explain a paradox of replication of large blocks of
monotonic repeats in a mammalian centromeres.

The utility of an alphoid DNA construct for analysis of the kinetohore structure
and gene expression depends on how easily the construct can be modified before
transfection and how easily the HAC can be isolated from mammalian cells. The
15 disclosed constructs contain both YAC and BAC cassettes. The presence of the two
cassettes gives many advantages: a HAC construct can be easily modified in yeast by
homologous recombination as a YAC and isolated as a BAC DNA from bacterial cells
for transfection experiments. At the same time HAC sequences can be rescued from
human cells by *E. coli* or yeast spheroplast transformation to analyze HAC
20 rearrangements during its propagation. The opportunity to re-isolate HAC sequences
both as a YAC or a BAC is important because both cloning systems have limitations
and the sequences clonable in yeast can be unclonable in *E. coli* cells and vice versa.

2. Example 2. A Strategy for Isolating of Human Centromeric DNA from Rodent/Human Cells by TAR 25 Cloning

Centromeric regions are composed of different types of repetitive sequences and
represent approximately 10% of human genome. Despite their importance for
kinetohore study and for the construction of Human Artificial Chromosomes (HACs),
these regions remain poorly characterized by prior efforts. The main reason for this is
30 that long stretches of tandemly repeated centromere-specific DNA sequences could not
be cloned by a standard YAC or BAC cloning technique.

5 A TAR (Transformation-Associated Recombination) cloning technology has
been disclosed for the direct isolation of genes and chromosomal fragments of hundred
kilobases in size from euchromatic regions of mammalian genomes. The approach is
based on transformation of the yeast spheroplasts by a gently isolated total genomic
DNA along with a TAR vector containing sequences homologous to a region of
10 interest. The high selectivity of gene isolation by TAR is due to the omitting of a yeast
origin of replication (ARS-like sequence) from a vector. As a consequence, a
propagation of the TAR vector in yeast cells absolutely depends on acquisition of
human DNA fragments with ARS-like sequences that can function as an origin of
replication in yeast. These sequences are common in euchromatic regions
15 (approximately one ARS-like sequence per 30 kb) that allows rescue of a region as a 50
kb or bigger size fragment.

In contrast, the isolation of specific fragments from heterochromatic regions
(including centromeres and telomeres) cannot be accomplished by a routine TAR
technique. These regions contain large blocks of repetitive sequences lacking an ARS
20 consensus sequence. Disclosed is a new TAR-based cloning system that allows direct
isolation of large fragments of genomic DNA from heterochromatic chromosomal
regions lacking ARS-like sequences. Figure 1 shows a scheme for the isolation of
centromeric regions by a new cloning system. In the new system an ARS element is
included into a TAR vector. To avoid a high background resulting from re-
25 circularization of an ARS-containing vector during yeast transformation (Noskov et al.,
Nucl. Acids Res. 29: c32, s (2001)), a counter-selectable marker, SUP11, was included
between specific targeting sequences in the vector. SUP11 encodes an ochre suppresser
tRNA and even one copy of the gene is highly toxic for a prion-containing (psi-plus)
yeast strain. As a consequence, autonomously replicating plasmids carrying SUP11
30 transform yeast cells very poorly. In addition, SUP11 suppresses an ade2-101 mutation
in a host strain. Ade2-101 cells are red while in the presence of SUP11 they are white.

5

These two phenotypes (toxicity and color of the colony) provide selectivity of cloning. Simple vector re-circularization restores the SUP11 gene that would lead to a high level of cell lethality and change the color of the colonies to white.

Recombination between targeting sequences in the vector and genomic DNA fragments
10 (a centromeric fragment as shown in Figure 1) deletes SUP11 sequences from the vector. Such colonies will be red.

To demonstrate the utility of a new technique for cloning of heterochromatic chromosomal regions, alphoid DNA arrays from five human chromosomes (11, 13, 15, 22 and Y) were isolated as DNA fragments of hundred kilobases in size and physically
15 characterized. Table 1 summarizes size of isolates and their mapping by FISH. More detailed analysis was carried out for alphoid DNA arrays isolated from human chromosome 22 and the Y chromosome (DYq74). This array was isolated as a set of YAC/BAC clones from 100 kb to 250 kb. The inserts are composed by alphoid DNA only as can be seen after digestion by EcoRI. The digestion produces two main
20 fragments 2.8 and 2.9 kb in size. Sequencing of the alphoid DNA array has shown that the array consists of direct repeats of a 5.7 kb unit (each unit contains thirty four copies of an about 170 bp monomer) and inverted repeats of a 1.6 kb unit (the unit contains 10 copies of an about 170 bp monomer: seven copies in one direction and three copies in another direction). Comparisons of monomers in 5.7 kb and 1.6 kb units are shown in
25 Figure 3 and Figure 4 correspondingly. Figure 5 summarizes data on sequence homology between different alphoid DNA monomers isolated from the DYq74 derivative of chromosome Y. For this alphoid DNA array we have also shown the formation of HACs after its transfection into human cells. Formation of a HAC by alphoid DNA arrays isolated from the Y human mini-chromosome has been shown.
30 170 kb BAC was transfected into HT1080 human cells. Co-localization of centromere-binding proteins and alphoid DNA probe to HACs has been shown. Based on these results, the disclosed system allows a direct isolation of centromeric (as well as other

5 heterochromatic) regions from a mammalian genome for further structural/functional analysis and construction of a new generation of HACs. These general methods are

Selective cloning of human-specific alphoid DNA arrays from a rodent/human hybrid cell line as circular YACs is based on *in vivo* recombination in yeast. A mixture of DNA from hybrid cells and a linearized vector is presented to yeast spheroplasts.

10 The vector contains a yeast selectable marker (*HIS3*), a yeast centromere (*CEN*), a yeast origin of replication (*ARS*) and *alphoid DNA* repeats at each end. Homologous recombination between *alphoid DNA* sequences in the vector and a human centromeric region leads to establishment of a circular YAC. Since rodent DNA does not contain *human-specific alphoid DNA* repeats, there should be no recombination of the vector
15 with rodent DNA fragments. As a result, most of the yeast transformants contain circular YACs with human DNA inserts.

This TAR cloning system allows for isolation of centromeric regions that can not be cloned by standard techniques. A one day yeast transformation experiment may generate several hundred clones containing circular YACs with alphoid DNA inserts
20 which represents a library of a specific centromere alphoid sequences. Isolation of alphoid DNA by TAR cloning from hybrid cell lines is highly specific. The size of alphoid DNA arrays isolated by TAR cloning can be varied, from about 80 kb to more than 500 kb.

a) Preparation of TAR vector

25 TAR vector pVC-sat was purified by CsCl-ethidium bromide centrifugation and linearized by *Sma*I prior to transformation. The linearization yields molecules bounded by alpha-satellite sequences.

5

(1) Preparation of chromosome-sized DNA in solid agarose plugs for TAR cloning

Low-melting-point agarose plugs (each containing ~ 5 ug of genomic DNA) were prepared from normal human leucocytes or from rodent or chicken somatic hybrid cells carrying either human chromosome 5, chromosome 16, chromosome 22, chromosome Y, or a mini-chromosome derived from Y. The cultured cells ($\sim 5 \times 10^7$) were harvested by centrifugation, resuspended in 4.0 ml of EDTA mix (50 mM EDTA; 10 mM Tris-HCl, pH 7.5) and placed in a 42°C tempblock as 0.5 ml aliquots. An equal volume (0.5 ml) of 42°C 1% melted agarose (BRL LMP agarose), prepared in 125 mM EDTA pH 7.5, was mixed by vortexing with each sample. (The final concentration of agarose should be equal to 0.5%.) 60-100 μ l of the mixture was then gently placed in Ultra Micro tips (Fisherbrand, #21-197-2E). The tips were kept for 10-15 min. at 4°C until the agarose had completely solidified. Each tip was placed into a 6cc syringe luer and the plugs were released into a 50 ml corning tube by applying gentle pressure. The cells were lysed in NDS [500 mM EDTA; 10 mM Tris-HCl, pH 7.5; 1% N-lauroyl sarcosine pH 9.5; 5 mg/ml proteinase K (PK, BDH)] at 50°C for 48 hours (all plugs were covered completely during incubation). To remove traces of the proteinase K, the agarose plugs were extensively washed with TE containing 50 mM EDTA and 10 mM Tris-HCl, pH 7.5. [One time during an hour at 50°C, then cooled to room temperature and washed at least 5-10 times (1 hour each wash)]. Chromosomal size DNAs were stored in TE solution at 4°C. Transverse Alternating Field Electrophoresis (TAFE) was used for analyzing DNA size. Agarose plugs (each ~100 μ l) were treated with 1-2 units of agarase prior to spheroplast transformation.

5

(2) TAR cloning of centromeric regions

Spheroplasts, that enable efficient transformation, were prepared using a modified method previously described for standard YAC cloning (Kouprina and Larionov, *Current Protocols in Human Genetics* 1: 5.17.1-5.17.21 (1999)). An individual colony of a host yeast strain was inoculated in 50 ml of supplemented YPD broth (in a 500 ml flask) and grown overnight at 30°C with vigorous shaking to assure good aeration until an OD₆₆₀ of ~1.0 was achieved (the actual measurement is from 0.09 to 0.13 after diluting 1/10 in water). Cells were collected by centrifugation at 3,100 x g for 3 min. at 5°C and then washed once with 20 ml of sterile water followed by an additional washing with 20 ml of 1.0 M sorbitol. The cells were resuspended in 20 ml of SPEM (1.0 M sorbitol; 0.01 M Na phosphate, pH 7.5) containing 20 µl of zymolyase (20T) (10 mg/ml), 40 µl of beta-mercaptoethanol (14 M) and incubated at 30°C for ~ 20 min. with slow shaking. (The treatment time conditions varied depending on the zymolyase stock). The cells were checked for percent spheroplasts. (Zymolyase treated cells were diluted 1/10 in 1.0 M sorbitol and 1/10 in 2% SDS. The spheroplasts were determined to be ready when the difference between the two OD₆₆₀ readings is 3 to 7 fold). The cells were collected by a low centrifugation at 300-800 x g for 10 min., washed gently 2-3 times in 20 ml of 1.0 M sorbitol and resuspended gently in 2.0 ml of STC (1.0 M sorbitol; 10 mM Tris, pH 7.5; 10 mM CaCl₂). The spheroplasts are stable at room temperature for at least one hour. Agarose plugs were placed in DMSF (1:100 in 25 mM NaCl), incubated for 60 min. at room temperature and then washed twice in 25 mM NaCl for 60 min. at room temperature before transformation. One microgram of the linearized pVC-sat TAR vector (1-10 µl) and one agarose plug containing ~5 µg of genomic DNA were mixed, incubated at 68°C for 5-10 min. in order to melt agarose and then placed at 42°C for 10 min. The mixture

5 was incubated with one unit of agarase [10 μ l of ten-fold diluted enzyme (Boehringer Mannheim) in 25 mM NaCl] at 42°C for 15 min. 450 μ l of competent yeast spheroplasts were gently added to the DNA mixture and incubated for 10 min. at room temperature. Subsequently, 4.5 ml of PEG solution (20% PEG 8000; 10 mM Tris, pH 7.5; 10 mM CaCl₂) was gently added to the mixture, incubated for 10 min. at room
10 temperature and centrifuged for 10 min. at 600 x g at 5°C. The settled transformed spheroplasts were gently resuspended in 2.0 ml of SOS (1.0 M sorbitol; 6.5 mM CaCl₂; 0.25% yeast extract; 0.5% bactopectone), incubated for 40 min. at 30°C without shaking, then gently mixed with 8.0 ml of melted TOP agar (48°C) and quickly plated. The plates were kept at 30°C for 5-8 days until the transformants were visible.

15 (3) Characterization of YAC clones

TAR cloning experiments were carried out with genomic DNAs prepared five different monochromosomal hybrid cell lines. Approximately 1,000 His⁺ colonics were obtained for each DNA. To identify transformants containing centromeric DNA, the transformants were combined into 40 pools and examined by PCR. A pair of
20 primers was utilized that identifies an alphoid DNA sequence that is not present in a TAR vector. From five to twelve pools were identified that yielded PCR products specific to alphoid DNA for each genomic DNA. Individual clones containing alphoid DNA arrays were isolated from each pool for further analysis. To estimate the size of circular YAC isolates, agarose DNA plugs were prepared from individual transformants and exposed to a low dose of γ -rays (5 Krad) before TAFE analysis. A specific *alphoid*
25 *DNA* probe for detection of human YACs generated by TAR cloning vectors was used. The probe is a 120 bp fragment from the 3' end of the *alphoid DNA* monomere sequence that is omitted in the TAR vector described above. The *alphoid* probe was labeled with ³²P dCTP using PCR. Clones with a large blocks of alphoid DNA were
30 also analyzed by endonuclease restriction.

5

(4) Transfer of retrofitted YAC/BACs into E. coli cells

YAC isolates were retrofitted into BACs with a mammalian selectable marker using BRV1 vector. Low-melting-point agarose plugs were prepared from yeast transformants using a standard method (Kouprina and Larionov *Current Protocols in Human Genetics* 1: 5.17.1-5.17.21 (1999)).

10

Before electroporation into *E. coli* cells, the plugs were treated as follows. The plugs were washed 6 times in 1X TE (1 mM EDTA, 10 mM Tris-HCl, pH 8.0), for at least an hour the first 5 washes, and then overnight in 0.5X TE for the final wash. Then the plug (approximately 100 μ l) was melted at 68°C for 15 min., cooled to 45°C for 10 min., treated with 1.5 unit of agarase for 1 hour at 45°C and chilled on ice for 10 min.

15

The treated plug was diluted 1:1 with 0.5X TE. One microliter of the mixture was electroporated into 20 μ l of the *E. coli* DH10B competent cells (Gibco BRL) using a Bio-Rad Gene Pulser with the settings 2.5 kV, 200 oms, and 25 uF. Colonies were selected on LB plates containing chloramphenicol at a concentration of 12.5 μ g/ml.

(5) Preparation of BAC DNA from E. coli cells

20

TB medium (100 ml) containing 12.5 μ g/ml chloramphenicol was inoculated with an individual bacterial colony containing a BAC and grown overnight. The cells were collected at 4,000 x g for 20 min. at 4°C, resuspended in 10 ml of solution I (50 mM glucose; 25 mM Tris-HCl, pH 8.0; 10 mM EDTA) and lysed with 2.0 ml of freshly prepared solution of lysozyme (10 mg/ml in 10 mM Tris, pH 8.0). The lysed cells were mixed thoroughly by gently inverting the bottle several times with 20 ml of freshly prepared alkaline solution (0.2 N NaOH, 1.0% SDS) and stored at room temperature for 10 min. Then 20 ml of ice-cold acetic acid-containing solution (3.0 M potassium acetate; 5.0 M glacial acetic acid) was added and mixed by shaking the bottle several times before placing the sample on ice for 10 min. The bacterial lysate was centrifuged at 4,000 x g for 30 min. at 4°C. The supernatant was filtered through four layers of cheesecloth and mixed with 0.6 volume of isopropanol and stored for 10 min. at room temperature. The DNA was

30

5 recovered by centrifugation at 5,000 x g for 20 min. at room temperature. The DNA pellet was dissolved in 3.0 ml of TE (pH 8.0) and purified by a QIAGEN column. The BAC DNA was ethanol precipitated and resuspended in 200 µl of TE. 20 µl of DNA solution was usually used for physical analysis. General TAR procedures can be found in Kouprina, N. and Larionov V. Selective isolation of mammalian genes by TAR cloning,
10 *Current Protocols in Human Genetics* 1: 5.17.1-5.17.21 (1999) which is herein incorporated by reference.

3. Example 3. Vector for TAR cloning of centromeric DNA

The vector, pVC-sat, was constructed using the TAR vector pVC604 described
15 in Noskov et al., *Nucleic Acids. Res.*, 29(6):e32 (2001). The pVC604 vector contains yeast centromere (CEN) and yeast selectable marker (HIS3). The vector also contains a ColE1 bacterial origin of replication and Amp resistance gene. To generate the pVC-sat vector capable of cloning blocks of centromeric repeats the following steps were carried out: a) ~150 bp yeast ARS sequence, ARSH4, was cloned into a unique NsiI
20 site of pVC604 (position 1530); b) 60 bp alphoid DNA sequence was synthesized based on published alphoid DNA monomer consensus sequence; c) two copies of the 60 bp sequence corresponding to 5' end of an about 170 bp alphoid DNA consensus were cloned into a polylinker of pVC604 + ARSH4 as ApaI-ClaI and BamHI-SacII fragments. The alphoid targeting sequences were cloned in a vector in opposite
25 orientation because we previously demonstrated that if two identical targeting sequences are cloned as a direct repeat in a TAR vector there would be no capture of genomic DNA. Instead there is an efficient circularization of the vector by intramolecular recombination (Larionov et al., *Proc. Natl. Acad. Sci. USA* 93: 13925-13930, 1996); d) A 140 bp fragment containing SUP11 gene was PCR amplified from
30 yeast genomic DNA and cloned as a ClaI-Bam HI fragment between the two satellite targeting sequences. There is an unique SmaI site in SUP11. This site was used for

5

linearization of the vector before TAR cloning. The schematic of this vector is shown in Figure 1 and the sequence of this vector is shown in Figure 6.

4. Example 4. Isolation of genomic regions containing blocks of satellite repeats by TAR cloning

10

TAR cloning provides a unique opportunity to selectively isolate any region of human DNA. We have adopted TAR cloning for isolation of blocks of alphoid DNA from human centromeres. A series of circular TAR vectors containing different parts of the consensus satellite unit as targeting sequences in direct and inverted orientations were constructed as described herein in Examples 1 and 2. Homologous recombination between
15 satellite sequences in the vector and a human centromere should lead to establishment of circular YACs with inserts of different size (Fig. 1).

Genomic DNA was gently prepared from the MRC-5 human fibroblasts and presented to yeast spheroplasts along with FseI-linearized TAR vectors (SAT-CEN6-HIS3-SAT-Sup11) as described in Examples 1 and 2. Utilizing 5 µg of genomic DNA, 1 µg of
20 the vector and 2×10^9 spheroplasts, there were approximately 20-30 transformants per experiment. In 5 independent transformation experiments, 130 His⁺ transformants were obtained. All the transformants were checked for the presence of alphoid DNA by dot-hybridization using a Sat-probe as described in Larionov V., Kouprina N., Graves J., and
25 Resnick M. A. Specific cloning of human DNA as YACs by transformation-associated recombination. Proc. Natl. Acad. Sci. USA 93: 491-496, 1996. Since the Sat-probe has no homology to the TAR vector and targeting satellite sequences, it was indicative for the presence of alphoid DNA in TAR-YACs. Among 130 transformants, nearly 75% (98/130) contained alphoid DNA, suggesting a high selectivity of cloning of centromere DNA.
30 Intensity of the radioactive signal was different for different isolates, indicating the different number of satellite units in the inserts. For further analysis we chose the 60 His⁺ isolates with the biggest number of satellite units (based on the strongest radioactive

5 signals). First, to assure that recombination occurred between satellite sequences present in the TAR vector and satellite units of human centromere, the YAC ends were rescued in *E. coli* and sequenced. Sequence analysis showed that YAC ends consist exclusively of alphoid DNA units. Isolation of YAC ends by plasmid rescue: the YAC ends were isolated as described in (Methods in Molecular Biology Volume 54, YAC protocols, edited
10 by David Markie, p. 139-144); the DNA isolated from the yeast transformants containing YACs was digested by EcoRI; after ligation and electroporation into *E. coli*, the rescued plasmids (AmpR) were checked for the absence of inserts and then isolated for further sequence analysis. Secondly, to assign each isolate to a certain centromere, fluorescence *in situ* hybridization (FISH) analysis was carried out with yeast DNA prepared from each
15 independent transformant. FISH analysis showed that the satellite-positive isolates map to or near human centromeres, but in most cases we observed more than one signal which is consistent with a previous observation that some satellite sequences cross hybridize with different centromeres (Fig. 13, 15 and Table 1). To determine the size of the inserts, the YACs were characterized by CHEF separation of chromosome size DNAs followed by
20 probing with the Sat-probe. The size varied from 50 kb to 400 kb (Table 1). Some isolates contained more than one band that is in agreement with previous observations that blocks of satellite DNA are unstable in wild type yeast host strains. To determine if the inserts derive from different regions of centromere, the DNAs from yeast isolates were digested by HindIII, EcoRI or XbaI, gel separated and hybridized with Alu-, LINE- and Sat-probes.
25 Nine isolates from sixty were Alu and/or LINE positive (Table 1), suggesting that these isolates are likely from pericentromeric regions of centromere. Indeed, analysis of the unique sequences from the Alu and LINE positive fragments of clone 25 mapped on centromere 2 revealed that this clone derives from the 2p11.1 pericentromeric region (contig NT_022171.6; positions 1665802-1665119, for example). For further analysis, to
30 be certain what centromere the clones derive from, we TAR-cloned alphoid blocks from genomic DNA prepared from a monochromosomal hybrid cell line containing a single human chromosome 22 and characterized them in more detail (see below). Among 100 transformants analyzed, nearly 40% (39/100) contained alphoid DNA. The size of inserts

5 varied from 50 kb to 200 kb. FISH analysis assigned each isolate to the centromere of chromosome 22. Seven BACs were Alu-positive, suggesting that they derive from the pericentromeric region of centromere 22.

Thus, we concluded that TAR cloning is very effective in isolation of human centromere regions.

10 a) Rescue of blocks of satellite repeats of chromosome Y from minichromosome $\Delta Yq74$

We also isolated an alphoid DNA array from a $\Delta Yq74$ hybrid cell line containing a fragment of the Y human mini-chromosome (Brown et al., 1994; Heller et al., 1996). This mini-chromosome was generated by two rounds of telomere-directed chromosome
15 breakage (Barnett et al., 1993). One of the breakages that occurred within the centromeric array of alphoid satellite DNA deleted the entire long arm of the chromosome and thus generated a short arm acrocentric derivative, $\Delta Yq74$, composed of only 140 kb of alphoid DNA and the breakage construct. The resulting mini-chromosome was linear and sized at approximately 12 Mb.

20 Two different strategies were used to isolate the alphoid DNA array from genomic DNA of the $\Delta Yq74$ hybrid cell line. The first strategy was based on our observation that a targeted chromosomal region can be rescued directly (Kouprina et al., 1998). Briefly, if a targeted chromosomal region contains the minimum requirements for its propagation in
25 yeast cells (CEN, ARS and a selectable marker) it can be rescued as a YAC simply by transformation of the total genomic DNA into yeast spheroplasts and following selection for the marker. Because truncation of the chromosome Y was done with the vector containing a yeast cassette, we proposed that selection for the URA3 marker would result in isolation of the chromosome region(s) containing a 140 kb block of alphoid DNA plus a
30 flanking region in the form of linear or circular YACs. Two different scenarios for the rescue of this targeted region may be considered. The presence of multiple (TG)_n telomere-like sequences that are frequent in human DNA (approximately once per 40 kb)

5 and the human telomere at the end of the mini-chromosome would provide an opportunity for circularization through homologous recombination and lead to generation of circular YACs. Alternatively, healing only one broken end of the rescued chromosome fragment(s) in yeast by yeast-like telomeric repeats would lead to establishment of linear YACs. After transformation of yeast spheroplasts by genomic DNA isolated from the hybrid cell line
10 $\Delta Yq74$ and following selection for the URA3 marker, we obtained 20 Ura⁺ transformants containing linear YACs of different size from 100 kb to 250 kb that proved the second mechanism of rescue of the targeted region. The alphoid DNA array of $\Delta Yq74$ has been also isolated by a TAR cloning system allowing the cloning of genomic regions containing only monotonic repeats. A new TAR vector includes a yeast selectable marker (HIS3), a
15 yeast centromere sequence (CEN6), a yeast origin of replication (ARSH4) and alphoid DNAs as targeting sequences. To eliminate a plasmid background during a TAR cloning, a counter-selectable marker (SUP11) was incorporated between the alphoid DNA targeting sequences. Co-transformation of the vector and genomic DNA isolated from the $\Delta Yq74$ cell line resulted in rescue of the alphoid DNA array as circular 50- 250 kb YACs.

20 To prove that the rescued YACs originated from the centromere of chromosome Y, we have used fluorescence in situ hybridization, which provides a quick and direct method for localization of the YACs. Three YACs, 100 kb, 150 kb and 250 kb, chosen for this experiment exhibited one strong signal on the centromere of the chromosome Y under stringent conditions. FISH analysis was conducted, briefly as follows. FISH
25 was carried out according to the method described in Yang JW, Pendon C, Yang J, Haywood N, Chand A, Brown WR. Human mini-chromosomes with minimal centromeres. Hum Mol Genet. 2000 9:1891-1902. Cells were cultured as above, cultured to mid-log phase and colcemid added to 0.1 μ g/ml. Cells were cultured for a further 2-3 h and then harvested, swollen in hypotonic solution (40 mM KCl, 0.5 mM
30 Na₂EDTA, 20 mM HEPES, pH 7.4) for 10 min at 37°C, pelleted and fixed in methanol/acetic acid at -20°C. The nuclei were dropped onto microscope slides, dehydrated in ethanol, and denatured in 70% formamide, 2x SSC for 5 min at 70°C. Probes for hybridization were nick-translated with biotin-16-dUTP (Roche) and

- 5 hybridized in 50% formamide, 10% dextran sulphate, 2x SSC, 40 mM sodium phosphate pH 7.0, 1x Denhardt's solution, 0.5 mM Na₂EDTA, 120 µg/ml sonicated salmon sperm DNA at 42°C overnight. Biotin-labelled probe was detected with Cy3-conjugated avidin (Amersham Pharmacia Biotech, Little Chalfont, UK) and the signal was amplified with biotin-conjugated goat anti-avidin (Vector Laboratories, Peterborough, UK) and a second round of Cy3-conjugated avidin. Chromosomes and nuclei were counterstained with DAPI at 0.5 µg/ml.

b) Physical characterization of YAC/BACs containing blocks of satellite repeats from centromere of chromosome 22 and Y

15

- BACs have advantages versus YACs because they can be easily isolated by alkaline method for further analysis. Therefore, three circular YAC isolates containing alphoid DNA arrays from chromosome Y and eleven isolates from chromosome 22 were retrofitted by recombination in yeast with the vector BRV1 that contains sequences that would enable subsequent propagation in *E. coli* as BACs. These YAC/BACs were then transferred to *E. coli* by electroporation, as described herein. BAC DNAs from 10 independent *E. coli* transformants for each YAC/BAC were isolated, digested with NotI and CHEFgel separated to determine the size of BAC inserts after electroporation. Analysis has shown that for most clones the alphoid DNA BACs kept the same size as original YACs and were reasonably stable in bacterial cells. Digested BAC DNAs gave one major predicted size band. The fraction of deleted BAC forms (visible as minor bands on electrophoregrams) did not exceed 5% in DNA preparations.

- The alphoid DNA within the main block of chromosome Y is organized into tandemly repeating units, most of which are about 5.7 kb long. Each unit consists of 34 tandemly repeated 171 bp monomers of alphoid DNA and contains a single EcoRI site and a pair of XbaI sites (McDermid. In order to determine whether the isolated alphoid DNA arrays from ΔYq74 have the same organization, the BACs were digested with either EcoRI or XbaI, separated by gel electrophoresis and blot hybridization using a 5.7 kb alphoid

5 DNA fragment as a probe. The analysis has shown that inserts of 100 kb, 120 kb and 140 kb BACs consist exclusively of alphoid DNA. EcoRI digestions generated a main 5.7 kb fragment corresponding to alphoid DNA. The intensity of other fragments corresponding to a vector and junction between a vector and an insert was much less. Similar results were obtained with XbaI BAC digestions. During restriction analyses of the BACs we found
10 that the alphoid 5.7 kb DNA unit contains two SpeI recognition sites. Digestion of the BACs by SpeI produced two fragments with size 2.8 kb and 2.9 kb (Fig. 22). Because SpeI is a rare cutter enzyme, we supposed that SpeI digestion could be used to detect the chromosome Y-specific higher order alphoid sequences in genomic DNAs. Indeed, we observed only 2.8 kb and 2.9 kb fragments seen on electrophoregrams of the SpeI digests
15 of male genomic DNA. To conclude, our data indicate that in general the organization of alphoid DNA arrays in TAR YAC/BAC isolates are similar to that on centromere of chromosome Y.

The alphoid DNA within the main block of chromosome 22 is organized into tandemly repeating units, most of which are about 2.1 kb and 2.8 kb long. Each unit
20 consists of 12 and 16 tandemly repeated 171 bp monomers of alphoid DNA, respectively, and contains a single EcoRI site. The complete DNA sequences of 12 and 16 tandemly repeated units are shown in SEQ ID NO:53 and SEQ ID NO:54. The positions of the repeats in the 2.1 kb fragment are 1, 172, 342, 512, 683, 854, 1025, 1196, 1366, 1537, 1708 and 1888. The positions of the repeats in the 2.8 kb fragment are 1, 172, 342, 507,
25 678, 848, 1019, 1189, 1360, 1531, 1702, 1872, 2043, 2214, 2382 and 2553. The percent divergence between units was 78%. The structure of each repeating unit is readily discernable in the disclosed sequences. In order to determine whether the TAR-isolated alphoid DNA arrays have the same organization as on chromosome, the BACs were digested with EcoRI, separated by gel electrophoresis and blot-hybridized with a Sat-
30 probe. The analysis has shown that inserts of most of the BACs consist exclusively of alphoid DNA but the restriction profiles are different. For BACs 9, 11, 14, 19 and 35, EcoRI digestion generated two main fragments, 2.1 kb and 2.8 kb (Fig. 14), suggesting that these alphoid DNAs derive from a very monogenic array characteristic for higher order

5 structure. For BACs 3, 5, 6, 10, 15 and 20, EcoRI digestion generated multiple bands with periodicity of 171 bp, suggesting more diversity between satellite units (Fig. 20). Fluorescence in situ hybridization performed with BAC clones 14 and 5 showed hybridization signals on chromosome 22 only by metaphase FISH. Co-localization to the centromeric region suggested a possible overlap. To further define their relative physical
 10 position, a fiber FISH high resolution mapping was performed (Fig. 13). The result demonstrates some overlap of BACs 14 and 5 detecting one or probably two regions of hybridization for the BAC 14 (Spectrum Orange) within the long stretch of BAC 5 (Spectrum Green) that has a homology to the extended area of the centromere, most likely due to a presence of the chromosome 22 specific repeat(s).

15 c) Alphoid DNA contains ARS-like sequences that can function as origin of replication in yeast

ARS-like elements that act as an origin of replication in yeast are short (approximately 50 bp) AT-rich sequences containing a non-conserved 17 bp core
 20 consensus (Theis and Newlon 1997). Random clones with inserts from euchromatic genomic regions carry on average one *ARS*-like sequence in 20-40 kb (Stincomb et al., 1980) as detected by ability to transform yeast cells with a high efficiency. In contrast genomic regions corresponding to a large block of repeats such as alphoid DNA repeats in the centromere may not contain *ARS*-like sequences. To investigate the presence of *ARS*-
 25 like sequence in alphoid DNA arrays, alphoid DNA from TAR BAC clone 11 (chromosome 22) was digested by Sau3A and cloned into a URA3-CEN6 yeast vector, lacking an origin of replication. Two thousand randomly selected recombinant plasmids were purified from *E. coli* and transformed into yeast spheroplasts. Forty-eight clones exhibited a high transformation efficiency comparable to that for a yeast *ARS/CEN* vector,
 30 suggesting that these inserts contain an yeast origin of replication sequence(s). Indeed sequence analysis of these clones revealed several *ARS*-like elements corresponding to the published *ARS* consensus sequence WWWTTTAYRTT¹WDTT (Theis and Newlon 1997). All these sequences were located in positions 126-141 of an about 171 bp alphoid

- 5 DNA monomer (Figure 23 & SEQ ID NO:52). Because we did not find good matches to the ARS consensus sequence in each satellite unit, we conclude that presence of ARS-like elements is unlikely a general property of human alpha satellite DNA. In agreement with such conclusion, we failed to detect ARS-like sequences in alphoid DNA arrays isolated from Y human chromosome and $\Delta Yq74$ minichromosome.

10 d) Sequence analysis of alphoid DNA arrays

The complete sequence of a 5.7 kb alphoid DNA unit from chromosome Y was not available. Therefore, we subcloned the 2.8 kb and 2.9 kb SpeI fragments and determined nucleotide sequence of the entire unit. The sequences were divided into 171 bp monomers and aligned to maximize monomer similarity. Values of divergence were calculated for pair wise comparisons of all 34 monomers. The 5.7 kb unit contains type A monomers (pJa sites only), which is not surprising because the centromere of chromosome Y does not contain CENP-B binding sites (Table 2) (Cooper et al. 1993; Tyler-Smith et al., *Nat. Genet.* 5:368-375, 1993). These monomers are highly diverged: the average divergence from the consensus sequence is 0.116 (32% divergence). This is an example of absence of frequent homogenization events suggesting that they are not subject to concerted evolution (Nei et al., *Proc Natl Acad Sci USA* 97:10866-10871, 2000). A neighbor-joining phylogenetic tree (Fig. 5? Yes this is correct) shows that only a few monomers may have been duplicated relatively recently (e.g. pairs sat19 - sat22 and sat20 - sat23). A high level of divergence (between 12% and 30% for different monomers) explains why these blocks of alphoid DNA quite stably propagate both in yeast and *E. coli* hosts.

Sequence analysis of 2.1 kb and 2.8 kb units cloned from BAC11 containing alphoid DNA from chromosome 22 revealed that they also primarily contain type A monomers; there are only a few highly diverged B monomers (having CENP-B binding sites) found (Table 3). In contrast, satellite units from BAC5 that, based on restriction analysis, are not organized in higher order structure contain a mixture of A and B monomers (Table 3); this is a typical situation for autosomal alpha satellite DNA (reviewed by Alexandrov et al. 2001).

5 The BioEdit program was used for reconstruction of an entropy plot for monomers from the 5.7 kb alphoid DNA unit; in this plot smaller values of Hx correspond to a lower variability of a position. Interestingly, the CENP-B box (which is located at the very end of the alignment) does not have the lowest Hx value. The ARS-like element in positions 126-141 also has a number of highly variable positions (Fig. 9?).

10 e) Formation of a de novo centromere in human cells using the present HAC.

 A 140 kb insert from a TAR isolate containing the chromosome 22 alphoid DNA array lacking CENP-B boxes was retrofitted by a mammalian selectable marker (Neo) and was transfected into human HT1080 cells to evaluate formation of human artificial
15 chromosomes. Artificial chromosomes containing the chromosome 22 alphoid DNA array were generated in approximately 30% of clones, similar to that observed for other HAC constructs with alphoid DNA isolated from human chromosome 21 (Ebersole et al.,
 Hum. Mol. Genet., 9:1623-1632, 2000), chromosome 17 (Mejia et al., *Genomics* 79:297-304, 2002) and chromosome X (Schueler et al., *Science* 294:109-115, 2001). Analysis of
20 five such artificial chromosomes has shown that the HACs are mitotically stable in the absence of drug selection and each recruited a centromere protein, CENP-E that is associated with active centromere (Fig. 21). Minichromosome frequency in positive cell lines varied between 12 and 85% of metaphase spreads, and copy number was consistently low at one or rarely two minichromosomes per positive spread. We did not
25 observe integration of input DNA into the natural chromosomes. These data indicate that blocks of alphoid DNA from chromosome 22 lacking CENP-B boxes and containing a yeast ARS sequence are highly competent to form a de novo centromere. FISH analyses of the artificial chromosomes did not detect any non-alphoid DNA sequences, suggesting that HAC formation took place without an acquisition of the host DNA.

30

5 Throughout this application, various publications are referenced. The disclosures of these publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art to which this invention pertains, even if the reference is not specifically incorporated

10 It will be apparent to those skilled in the art that various modifications and variations can be made in the present invention without departing from the scope or spirit of the invention. Other embodiments of the invention will be apparent to those skilled in the art from consideration of the specification and practice of the invention disclosed herein. It is intended that the specification and examples be considered as exemplary only, with a true scope and spirit of the invention being indicated by the
15 following claims.

5. Summary of Sequences

20 List of sequences SEQ ID NO:1 is a 1.6 kb fragment of the Y chromosome; SEQ ID NO:2 is a 2.8 kb major Spe I fragment of $\Delta Yq74$; SEQ ID NO:3 is a 2.9 kb major Spe I fragment of $\Delta Yq74$; SEQ ID NOs:4-37 are approximately 170 base alpha satellites of the Y Chromosome; SEQ ID NOs:38-42 are approximately 170 base alpha satellite repeats of a 1.6 kb fragment of $\Delta Yq74$; SEQ ID NOs: 43-46 are inverted repeats from a 1.6 kb fragment of $\Delta Yq74$; SEQ ID NOs:47-50 are PCR primers from Example1; SEQ ID NO: 51 is the sequence of TAR cloning vector as shown in Figure 6; SEQ ID NO:52 is the sequence of the ARS of chromosome 22 as shown in Figure
25 23; SEQ ID NO:53 is a 2.1 kb fragment of chromosome 22; and SEQ ID NO: 54 is a 2.8 kb fragment of chromosome 22.

What is claimed is:

1. A mammalian artificial chromosome comprising the structure Y-X-Z-Y, wherein Z comprises a sequence less than about 250 kb and which is capable of correctly segregating the mammalian artificial chromosome.
2. A mammalian artificial chromosome comprising the structure Y-X-Z-Y, wherein the mammalian artificial chromosome can be shuttled between bacteria, yeast, and mammalian cells without alteration of the mammalian chromosome.
3. A mammalian artificial chromosome comprising the structure Y-X-Z-Y, wherein Z comprises an inverted repeat sequence.
4. The mammalian artificial chromosome of claims 1, 2, or 3, wherein Z further comprises a sequence less than about 150 kb.
5. The mammalian artificial chromosome of claims 1, 2, or 3, wherein Z further comprises a sequence less than about 100 kb.
7. The mammalian artificial chromosome of claims 1, 2, or 3, wherein Z further comprises a nucleic acid sequence that lacks a functional CENP-B box sequence.
8. The mammalian artificial chromosome of claims 1, 2, or 3, wherein Z further comprises alphoid DNA.
9. The mammalian artificial chromosome of claim 8, wherein the alphoid DNA consists of 34 repeats.
10. The mammalian artificial chromosome of claim 8, wherein the alphoid DNA is derived from the Y-chromosome centromere.
11. The mammalian artificial chromosome of claims 1, 2, or 3, wherein Z comprises a repeat structure of about 2.1 kilobases.
12. The mammalian artificial chromosome of claim 11, wherein Z further comprises a repeat structure of about 2.8 kilobases.

13. The mammalian artificial chromosome of claims 1, 2, or 3, wherein the Z comprises a sequence having at least 70% homology to SEQ ID NO:53 and a sequence having at least 70% homology to SEQ ID NO:54.

14. The mammalian artificial chromosome of claims 1, 2, or 3, wherein the Z comprises a sequence having at least 80% homology to SEQ ID NO:53 and a sequence having at least 80% homology to SEQ ID NO:54.

15. The mammalian artificial chromosome of claims 1, 2, or 3, wherein the Z comprises a sequence having at least 90% homology to SEQ ID NO:53 and a sequence having at least 90% homology to SEQ ID NO:54.

16. The mammalian artificial chromosome of claims 1, 2, or 3, wherein the Z comprises a sequence having at least 95% homology to SEQ ID NO:53 and a sequence having at least 95% homology to SEQ ID NO:54.

17. The mammalian artificial chromosome of claims 1, 2, or 3, wherein the DNA further comprises alphoid DNA derived from the 22-chromosome centromere.

18. The mammalian chromosome of claims 1, 2, or 3, wherein the chromosome is less than or equal to 10 MB.

19. The mammalian chromosome of claims 1, 2, or 3, wherein the chromosome is less than or equal to 5MB.

20. The mammalian chromosome of claims 1, 2, or 3, wherein the chromosome is less than or equal to 1MB.

21. The mammalian chromosome of claims 1, 2, or 3, wherein the chromosome is less than or equal to 750kb.

22. The mammalian chromosome of claims 1, 2, or 3, wherein the chromosome is less than or equal to 300 kb.

23. The mammalian chromosome of claims 1, 2, or 3, wherein the chromosome is less than or equal to 100 kb.

24. The mammalian chromosome of claims 1, 2, or 3, further comprising a yeast origin of replication.

25. The mammalian chromosome of claims 1, 2, or 3, wherein the chromosome is derived from a human chromosome.

26. A method of using the chromosome of claims 1, 2, or 3, comprising transfecting the chromosome into a mammalian cell producing a transfected cell.

27. The method of claim 26, further comprising culturing the transfected cell.

28. The method of claim 27, further comprising isolating the chromosome from the transfected cell.

29. The method of claim 28, further comprising transfecting the cell into a yeast cell.

30. The method of claim 28, further comprising transfecting the cell into a bacterial cell.

31. A method of using the chromosome of claims 1, 2, or 3, comprising transfecting the chromosome into a yeast cell producing a transfected cell.

32. The method of claim 31, further comprising culturing the transfected cell.

33. The method of claim 32, further comprising isolating the chromosome from the transfected cell.

34. The method of claim 33, further comprising transfecting the cell into a mammalian cell.

35. The method of claim 33, further comprising transfecting the cell into a bacterial cell.

36. A method of using the chromosome of claims 1, 2, or 3, comprising transfecting the chromosome into a bacterial cell producing a transfected cell.

37. The method of claim 36, further comprising culturing the transfected cell.

38. The method of claim 37, further comprising isolating the chromosome from the transfected cell.

39. The method of claim 38, further comprising transfecting the cell into a yeast cell.

40. The method of claim 38, further comprising transfecting the cell into a mammalian cell.

41. A shuttle vector comprising the mammalian artificial chromosome of claims 1, 2, or 3.

42. A cloning vector having the sequence set forth in SEQ ID NO:53.

43. A cloning vector having the sequence set forth in SEQ ID NO:54.

Selective Isolation of a Centromeric Region by TAR Vector with a Counter-selectable Marker

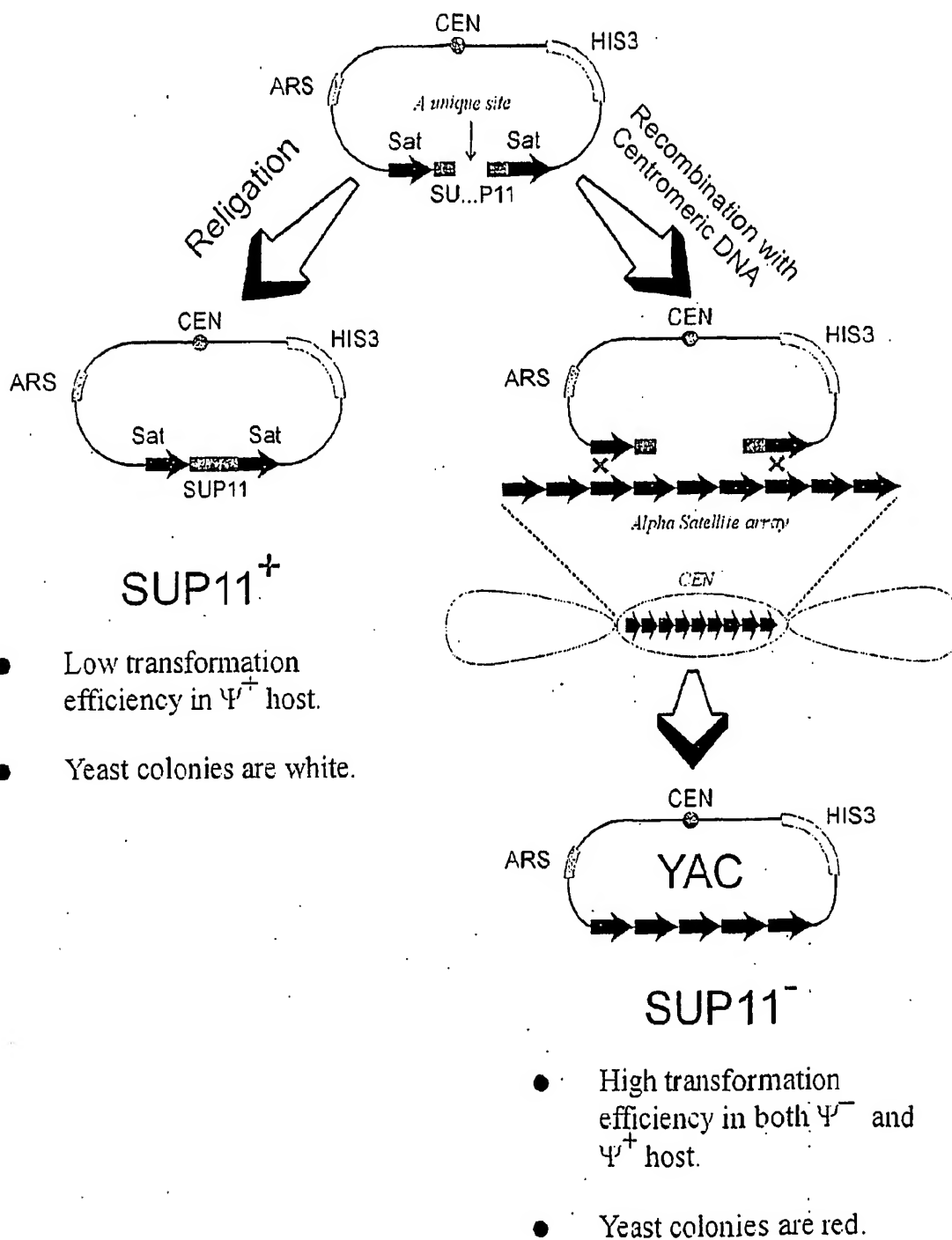


FIG. 1

**Organization of Alphoid DNA Array in Centromere
Region of Human Chromosome Y**

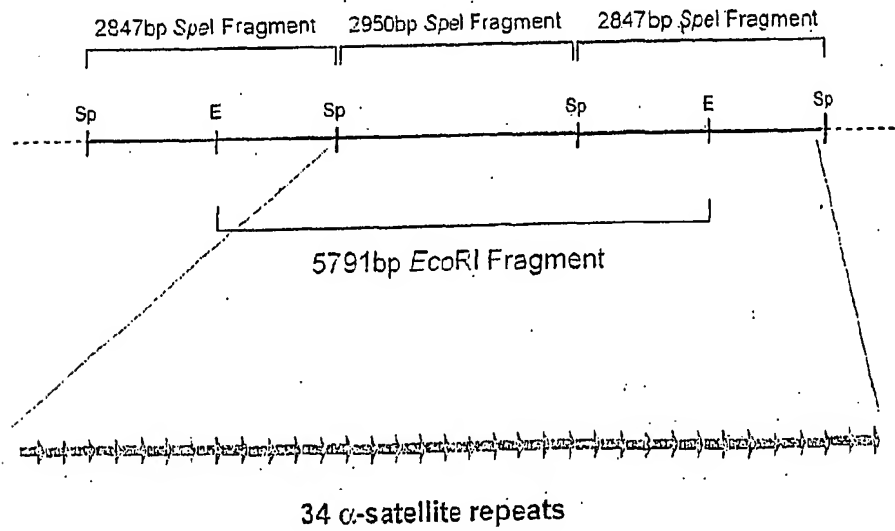


FIG. 2

		10	20	30	40	50	
Alpha 1	1	AGGCGTCAAA	GTGCTGCAAA	TATTCACCTG	TACATTCTAG	CAAAAG-AGT	50
Alpha 2	1	AGCGTGCAAA	AGGCTTCAAA	TATGGCCCTT	GAGATTCCAG	AAAAAG-AGT	50
Alpha 3	1	AGCGCGCAAT	GTACTCCAAA	TATCCAGCTG	CAGATTCTAG	-AAAAG-TGA	50
Alpha 4	1	AGGTCTCAAA	CCACTCCAAA	TATCCACTTG	TAGATTCTAT	AAAAAG-GAA	50
Alpha 5	1	GGGCGCAGAA	GGGCTCCAAA	TATCCACTTG	CAGATTCTAG	AAAAAG-AGA	50
Alpha 6	1	ACTCCACAAA	GTGCTGCAAA	TATCCACTTA	CATATTCTAG	AAAAAG-ATT	50
Alpha 7	1	AGGTCTTAAA	ACGCTCCAAA	TATCCACTTG	CAGATTCTAT	AAAAAG-ATT	50
Alpha 8	1	AGGCTGCAAA	GGGCTGCAAA	TATCCACTTG	CAGATTCTAT	AAAAAG-ATT	50
Alpha 9	1	AGTTCTCAAA	CCACTGCAAA	TATCCACTTG	CAGATTCTAG	AAAAAG-AGT	50
Alpha10	1	AGATCCGCAG	GGGACACAAA	TATCCACTTG	CAGATTCTAG	AAAAAG-AGA	50
Alpha11	1	AGACGTCAAA	GTGATGCAAA	TATCCACTTG	CAGATTCTAG	AAAAAG-AGT	50
Alpha12	1	AGGCTGCAAA	GGGCTGCAAA	TATCCACTTG	CAGATTCTAG	AAAAAG-AGT	50
Alpha13	1	AGAGCCGAAA	AGGCTGCAAA	TATTCACCTG	CAGATTCTAA	AAAAAG-AGT	50
Alpha14	1	AGGCTGCAAA	AGGCTGCAAA	TATTCACCTG	CAGATTCTAT	AAAAAG-AGA	50
Alpha15	1	TGGCTCAAA	AT-TTTCAAA	TATTCACCTG	CAGATTCTAG	AAAAAG-AGT	50
Alpha16	1	AGGCTGCAAA	GTGCTGCAAA	TATTCACCTG	CAGATTCTAG	AAAAAG-AGT	50
Alpha17	1	AGGCGGCAAA	GGGCTGCAAA	TATTCACCTG	CAGATTCTAG	AAAAAG-AGA	50
Alpha18	1	CTTCCACAAA	GGTCTGCAAG	TATTCACCTG	CAGATTCTAG	AAAAAG-AGA	50
Alpha19	1	AGGCTGCAAA	GGGCTGCAAA	TATTCACCTG	CAGATTCTAG	AAAAAG-AGA	50
Alpha20	1	AGGCTGCAAA	GTGCTGCAAA	TATTCACCTG	CAGATTCTAG	AAAAAG-AGA	50
Alpha21	1	AGGCTGCAAA	GGGCTGCAAA	TATTCACCTG	CAGATTCTAG	AAAAAG-AGA	50
Alpha22	1	AGGCTGCAAA	GGGCTGCAAA	TATTCACCTG	CAGATTCTAG	AAAAAG-AGA	50
Alpha23	1	AGGCTGCAAA	GGGCTGCAAA	TATTCACCTG	CAGATTCTAG	AAAAAG-AGA	50
Alpha24	1	AGGCTGCAAA	GGGCTGCAAA	TATTCACCTG	CAGATTCTAG	AAAAAG-AGA	50
Alpha25	1	AGGCTGCAAA	GGGCTGCAAA	TATTCACCTG	CAGATTCTAG	AAAAAG-AGA	50
Alpha26	1	AGGCTGCAAA	GGGCTGCAAA	TATTCACCTG	CAGATTCTAG	AAAAAG-AGA	50
Alpha27	1	AGGCTGCAAA	GGGCTGCAAA	TATTCACCTG	CAGATTCTAG	AAAAAG-AGA	50
Alpha28	1	AGGCTGCAAA	GGGCTGCAAA	TATTCACCTG	CAGATTCTAG	AAAAAG-AGA	50
Alpha29	1	AGGCTGCAAA	GGGCTGCAAA	TATTCACCTG	CAGATTCTAG	AAAAAG-AGA	50
Alpha30	1	AGGCTGCAAA	GGGCTGCAAA	TATTCACCTG	CAGATTCTAG	AAAAAG-AGA	50
Alpha31	1	AGGCTGCAAA	GGGCTGCAAA	TATTCACCTG	CAGATTCTAG	AAAAAG-AGA	50
Alpha32	1	AGGCTGCAAA	GGGCTGCAAA	TATTCACCTG	CAGATTCTAG	AAAAAG-AGA	50
Alpha33	1	AGGCTGCAAA	GGGCTGCAAA	TATTCACCTG	CAGATTCTAG	AAAAAG-AGA	50
Alpha34	1	AGAATGCAAA	GGGCTGCAAA	TATTCACCTG	CAGATTCTAG	AAAAAG-AGA	50

FIG. 3A

		60	70	80	90	100	
Alpha 1	51	ATTTTCAAAC	TGCTCAA-TC	AAATGCAACG	TTCAAACCG	TGACATGAAT	100
Alpha 2	51	GTTTTCAAAC	TACTCAAATC	AAAAAATGAT	TTCAACTCTG	TGAGATGAAT	100
Alpha 3	51	GTTTTCAAAC	TGCTCTA-TC	AAAGATCAG	TTGGTCTCTG	TGAGTTGAAT	100
Alpha 4	51	TGTTTCAANT	TGCTCAA-TC	AAATAAAGT	TTCAACACCG	TGAGTGAGT	100
Alpha 5	51	GTTTTCAACAC	TGCTCTA-TC	AAACAATATG	TTCAACTTTG	TGGGTGCAAC	100
Alpha 6	51	GCTTTCGAAAC	TGCACAA-TC	AAAGAAAGG	TTCAATATA	TGAGTGAAT	100
Alpha 7	51	GTTTTCAAAC	TGCACAA-AA	AAA-GAATG	TTCAATCTG	TTTGTGAAT	100
Alpha 8	51	ATTTTCAAAC	TGCTCAA-TC	ATAGGAAATG	TTCAACTCTG	TGAGATGAAT	100
Alpha 9	51	ATTTTCAAAC	TGCTCAA-TC	AAAGAAAGG	TTCAACTCTG	TGAGATGAAT	100
Alpha10	51	GGTTTCAAAC	TAGTCAA-TC	AAGGATGGT	TTCAACTATG	TGAGTTGAAT	100
Alpha11	51	GTTTTCAAAC	TGCACAA-CC	AAAGAAAGG	TTCAACTAGG	TGAGATGAAT	100
Alpha12	51	GTTTTCAAAC	TGCTCAA-TC	AAAGAAAGA	TTTAACCTG	TGAGATGAAT	100
Alpha13	51	GTTTTCAAAC	TGCTCAA-TC	AAAGATAG-	TTCAACTCTG	TGAGAAAGAT	100
Alpha14	51	GTTTTCAAAC	TGCTCAT-TC	AAATATAGG	TTCAACTCTG	TGGTTTGAAT	100
Alpha15	51	GTTTTCAAAC	TGCTCTA-TC	AAATA--AAG	TTCAACTCTG	TGAGTTGAAT	100
Alpha16	51	GTTTTCAAAC	TGCTCAA-TC	AAAGAAAGG	TTGCACTCTG	GGAAATTAT	100
Alpha17	51	GTTTTCAAAC	TGCTCTA-CC	AAAGATAGG	TTCAACTCTG	TGAGTTGAAT	100
Alpha18	51	GTTTTCAAAC	TGCTCTA-TC	AAAGATCAG	TTCAACTCTG	TGGTTTGAAT	100
Alpha19	51	TTTTTCAAAC	TACTCAA-TC	AAAGAAAGG	TTCAACTCTG	TGAGTTGAAT	100
Alpha20	51	GTTTTCAAAC	TGCTCAA-TC	AAGAGCAAGT	TTCAAGTCTG	TGAGCTGAAT	100
Alpha21	51	GTTTTCAAAC	TGCTCTA-TC	AAAGATAGG	TTCAACTATG	TGATATGAAT	100
Alpha22	51	TTTTTCAAAC	TATTCAA-TC	AAAGAAAGG	TTCAACTCTG	TGAGTTGAAT	100
Alpha23	51	GTTTTCAAAC	TGCTCAA-TC	AAGAGCAAGT	TTCAAGTCTG	TGAGGTGAAT	100
Alpha24	51	GTTTTCAAAC	TGCTCTA-TC	AAAGATAGG	TTCAACTCTG	CGAGTTGAAT	100
Alpha25	51	TTTTTCAAAC	TTGTCAA-TC	AAAGCAAGG	TTCAACTCTG	TGAGTTGAAT	100
Alpha26	51	TTTTTCAAAC	TGCTCAA-TC	AAAGATAGG	TTCAACTCTG	TGAGTTGAAT	100
Alpha27	51	GTTTTCAAAC	TGCTCTA-TC	AAAGATAGG	TTCAACTCTG	AGAGTTTGAAT	100
Alpha28	51	GTTTTCAAAC	TGCTCTA-TC	AAAGATAGG	TTCAACTCTG	TGAGTTGAAT	100
Alpha29	51	GTTTTCAAAC	TGCTCTA-TC	AAAGATAGG	TTCAACTCTG	--AGAGTTGAAT	100
Alpha30	51	GTTTTCAAAC	TGCTCTA-CC	AAAGATAGG	TTCAACTCTG	TGAGTTGAAT	100
Alpha31	51	GTTTTCAAAC	TGCTCTA-TC	AAAGATAGG	TTCAACTCTG	TGAGTTGAAT	100
Alpha32	51	CTTTTCAAAC	TGCTCAA-TC	AAAGAGACA	TTCAACTCTG	TGAGTTGAAT	100
Alpha33	51	GTTTTCAAAC	TACTCAA-AC	AAAG---	TTCAACTCTG	TGAGTTGAAT	100
Alpha34	51	TTTTTCAAAC	CGCTCTA-TC	AAAGTATAGG	TTCAACTCTG	TGAGTTGAAT	100

FIG. 3B

		110	120	130	140	150	
Alpha 1	101	GGCCACATCA	CAAAGTAGTT	TCTGAGAAATG	CTTCTGTGTA	GTMTTATGT	150
Alpha 2	101	GCACACATCA	CAAAGTAGTT	TCTGAGAAATG	TTCCTGCTG	GTTCCTATGC	150
Alpha 3	101	GCATACATCA	AAAGGASCT	TCTGAAATG	CTTCTGTGTA	GTMTTCCGT	150
Alpha 4	101	GCACAAATCA	CAAAGGAGTT	TCTGAAATG	CTTCTGTGTA	GTMTTCTGT	150
Alpha 5	101	ACAAATATCA	CAA-GAATTT	TCTCCAAATG	CTTCTGTGTA	GTMTTATGT	150
Alpha 6	101	GCACACATCA	CAAAGAAGTT	TCTGAGAATC	TCTCTGTGTA	ATTTTATGT	150
Alpha 7	101	GCACACATCA	CAAAGAAGTT	AGTGAAGATG	CTTCTGTGTA	GTMTTATGT	150
Alpha 8	101	GCACACATCA	CAA-GAATTT	TCTGAGAAATC	CTTCTGTGTA	GTMTTATGA	150
Alpha 9	101	GCACACATCA	CAAAGAAGTT	TCTGAGAATG	CTTCTGTGTA	GTMTTATGT	150
Alpha10	101	GCACACATCA	CAAGGACTA	TGTGCGAATT	CTTCTGTGTA	GTMTTATGT	150
Alpha11	101	GCACACATCA	GAAGGAAGTT	TCTGAGAATG	CTTCTGTGTA	GTMTTATGT	150
Alpha12	101	CCACACATCA	CAAAGAAGTT	TCTGAGAATG	CTTCTGTGTA	GTMTTATGT	150
Alpha13	101	GCACACATCA	CTCAGAAGTT	TCTGAGAATG	CTTCTGTGTA	GTMTTATAT	150
Alpha14	101	GCACACATCA	CAAGAAGTT	TCAGAAGATG	TCTCTGTGTA	GTMTTATGT	150
Alpha15	101	GCACACAGCA	CAAAATGCTT	TCTGAGAATG	CTTCTGTGTA	GTMTTATAT	150
Alpha16	101	GCACACATCT	CAAGGAGTT	TCTGAG---	CTTCTGTGTA	GTMTTATGT	150
Alpha17	101	GCACACATCA	CAAAGAAGTT	TCTGAGAATG	CACTGTGTA	GTMTTATGT	150
Alpha18	101	GCACACATCA	CAAGGATTT	TCTGAGATG	CTTCTGTGTA	GTMTTATAT	150
Alpha19	101	GCACATATCA	CAAAGAGTT	TCTGCGAATG	CGCTGTGTA	GTMTTATGT	150
Alpha20	101	GCACACATCA	AAAGTAGTT	TCTGAGAATG	CTTCTGTGTA	GTMTTATGT	150
Alpha21	101	GCACACATCA	CAAGTAGTT	TCTGAGATG	CTTCTGTGTA	GTMTTATGT	150
Alpha22	101	GTACATATCA	CAAAGAGTT	ACTGGAATG	CTTCTGTGTA	GTMTTATGT	150
Alpha23	101	GCACACATTA	CAAGGAGTT	ACTGGAATG	CTTCTGTGTA	GTMTTATGT	150
Alpha24	101	AAGGATATCA	CAAAATAGTT	TCTGCGAATG	CTTCTGTGTA	GTMTTATGT	150
Alpha25	101	GCACACATCA	CAGAGAGTT	TCTGGAATG	TTCCTGTGTA	GTMTTATGT	150
Alpha26	101	GCACACATGT	CAAGAAAGTT	TCTGAGAATG	CTTCTGTGTA	GTMTTATGT	150
Alpha27	101	GCACACATCG	TGAGAAGTT	TCTGAGAATG	CTTCTGTGTA	GTMTTATGT	150
Alpha28	101	ACACACATCA	CAAGGAGTT	TCTGAGAATG	CTTCTGTGTA	GTMTTATAT	150
Alpha29	101	ACACATCTCA	AAAGTAGTT	TCTGAGAATG	CTTCTGTGTA	GTMTTATGT	150
Alpha30	101	--A-AGATCA	CAAGGAGTT	TCTGAGAATG	CTTCTGTGTA	GTMTTATGT	150
Alpha31	101	GCACACATTA	CAAGGAGTT	TCTGAGAATG	CTTCTGTGTA	GTMTTATAT	150
Alpha32	101	GCACACATCG	TAAAGAGTT	TCTGAGAATG	CTTCTGTGTA	GTMTTATGT	150
Alpha33	101	GCACACATCA	CAAGGAGTT	TCTGAGAATG	CTTCTGTGTA	GTMTTATGT	150
Alpha34	101	ACACACATCA	CAAGGAGTT	TCTGAGAATG	CTTCTGTGTA	GTMTTATGT	150

FIG. 3C

		160	170	180	190	200
Alpha 1	151	GAAGATATTT	CCCTTTCCAG	ATC	200
Alpha 2	151	GAAGATAGTT	CCCTTTTCAC	GAT	200
Alpha 3	151	GAAGATAGTT	GTCTTTCTAC	GAT	200
Alpha 4	151	GAAGATAGTT	CCCTTTCTAC	CAT	200
Alpha 5	151	GAAGACATTT	CTTTTCCCTG	CAT	200
Alpha 6	151	GAAGATATTT	CCCTTTCCAC	CIT	200
Alpha 7	151	GAAGATATTT	CCCTTTCCAC	AAT	200
Alpha 8	151	GAAGATATTT	CCCTTTCCAC	AAT	200
Alpha 9	151	GAAGATATTT	G-TTTCAC	CAT	200
Alpha10	151	GAAGATATTT	CCCTTTCCAC	AAT	200
Alpha11	151	GAAGATATTT	CCCTTTCCAC	CAT	200
Alpha12	151	GAAGATATTT	CCCTTTCCAC	AAT	200
Alpha13	151	GAAGATATTT	CCCTTTCCAC	CGT	200
Alpha14	151	CCGATAGTTT	CCCTTTCCAC	CAT	200
Alpha15	151	GAAGATAGTT	CCCTTTCCAC	AAT	200
Alpha16	151	GAAGTATTTT	CCCTTTCCAC	AAT	200
Alpha17	151	GAAGACATTT	CCCTTTCCAC	CAT	200
Alpha18	151	GAAGATATTT	CCCTTTCCAC	CAT	200
Alpha19	151	GAAGATATTT	CCCTTTCCAC	AAC	200
Alpha20	151	GAAGATAGTT	CCCTTTCCAC	CAT	200
Alpha21	151	GAAGATATTT	CCCTTTCCAC	CAT	200
Alpha22	151	GAAGATATTT	CCCTTTCCAC	AAC	200
Alpha23	151	GAAGATATTT	CCCTTTCCAC	CGC	200
Alpha24	151	GAATATATTT	CCCTTTCCAC	CAT	200
Alpha25	151	GAAGATATTT	CCCTTTCCAC	AAT	200
Alpha26	151	GAAGATATTT	CCCTTTCCAC	CAT	200
Alpha27	151	GAAGATATTT	CCCTTTCCAC	CAT	200
Alpha28	151	GAAGATATTT	CCCTTTCCAC	CAT	200
Alpha29	151	GAAGATATTT	CCCTTTCCAC	CAT	200
Alpha30	151	GAAGATATTT	CCCTTTCCAC	AAT	200
Alpha31	151	GAAGATATTT	CCCTTTCCAC	AAC	200
Alpha32	151	GAAGATATTT	CCCTTTCCAC	CAT	200
Alpha33	151	GAAGATATTT	CCCTTTCCAC	GT	200
Alpha34	151	GAAGATATTT	CCCTTTCCAC	CAT	200

FIG. 3D

ACTAGTTTCTCAGAAATGTTTCTGCTGCTGCTCCTATGCGAAGATAGTTCCTTTTTCACCATAGGCCCGCAATGTACTCTCCAAA
 TATCCACCTGCGAGATTCTACAAAAGTGAATTTTCAAACTGCTCTATCAAAAGATCAGTTTCGTCCTCTGTGAGTTGAATGCCA
 TACATCAAAAAGAAGCTTCTCAAAATGCTTCTGTGTGTTTTCGGTGAAGATAGTTCCTTTTCTACCATAGGTCTCTCAAA
 CCACCTCCAAATATCCACCTTGTAGATTCTATAAAAAGGAATGTTCAAAATTTGCTCAATAAAAAATAAAGTTTCAACACCGGTG
 AGATGAGTGCACAAATCACAAGGAGTTTCTCAAAATGCTTCTGCGGTAGTTTTCTGTGGAAGATAGTTCCTTTTCTTCTACCA
 TGGGGCCACAAAGGGCTCCAAATATACCCACTTTCGAGATTCTACAAAAAGAGAGATTTCACAACTGCTCTATCAAAACAATATGT
 TCAACTTTTGTGGGTTGAACACAAATATCACAAGAAATTTTCTCCCAATGCTTCTGTGTAGTTTTATATGTGAAGACATTTCT
 TTTCCCTCCATAGTCCACAAAAGTGTCTCCAAATATCCACTTACATATTTCTAGAAAAAGATTGCTTTGGAAAACTGCACAAATGA
 AAAGAAAGGTTTCAAAATATATGAGATGAATGCACACATCACAAGAAAGTTTCTCAGAAATCTCTCTGTGTAAATTTTATATGTG
 AAGATATTTTCCCTTTCCACCTTAGGTCTTTAAAAACGGCTCCAAATATCCACTTTCGAGATACCTACAAGAAAGATTGTTCAAAAA
 CTGTCACAAAAAAGAAATGTTTCMAATTTCTGTTTGTGNTGANTGCACATCACAAGAAAGTTTCTCAGAAATGCTTCTCTGTAG
 TTTTATATGTGAAGATATTTTCTTTTCCACAAATAGGCCCTCAAAAGGCTTCCAAATATCCACTTCCAGATTTCTATGAAAAAGAA
 TATTTCCAAACGTCTCAATCATAGGAAATGTTTCAACTCTGTGAGATATGTAAGTGGATATTTTGGAGCACTTTTGTGGACTA
TGGAGGGAAAAAGAAATGTTCTTCAATAAAAACTACACAGAAAGCAATTTGGGAGAAAAATTTCTTGTGATATTTTGTGTTTCAACCC
ACAAAGTTGAACATATTTGTTTGTATAGAGCAGTTTGTGAAAACTCTCTTTTGTAGAAATCTGCAAGTGGGTATTTTGGAGCCCT
TTGTGGCCCATGTTAGAAAAGGAACATATCTTTCACAGAAAAAACTACCCAGAAAGCAATTTTGGAGAAAACTCCTTTTGTGATTTTGT
GCACATCTCACGGTGTGAAACCTTTATTTTATTTGAGCAATTTTGAACATTTCTTTTATAGAAATCTACAAGTGGATA
TTTGGAGTGGTTTGGAGACCTATGGTAGAAAAAGAACTATCTTTCACCCGAAAAACCCACACAGAAAGCAATTTTGGAGAACTTCT
TTTTGATGATGCATTTCAACTCACAGAGACGCACTGATCTTTTGTATAGACAGATTTTGGAACTCAGCTTTTGTAGAAATCTG
CAGGTGGATATTTGGAGTACATTTGGGGCCCTATGGTGAATAAAAGGAACATATCTTTCGCATGAGAAACCCAGGCAGAAAC

FIG 4

Alpha Satellite Phylogenetic Tree

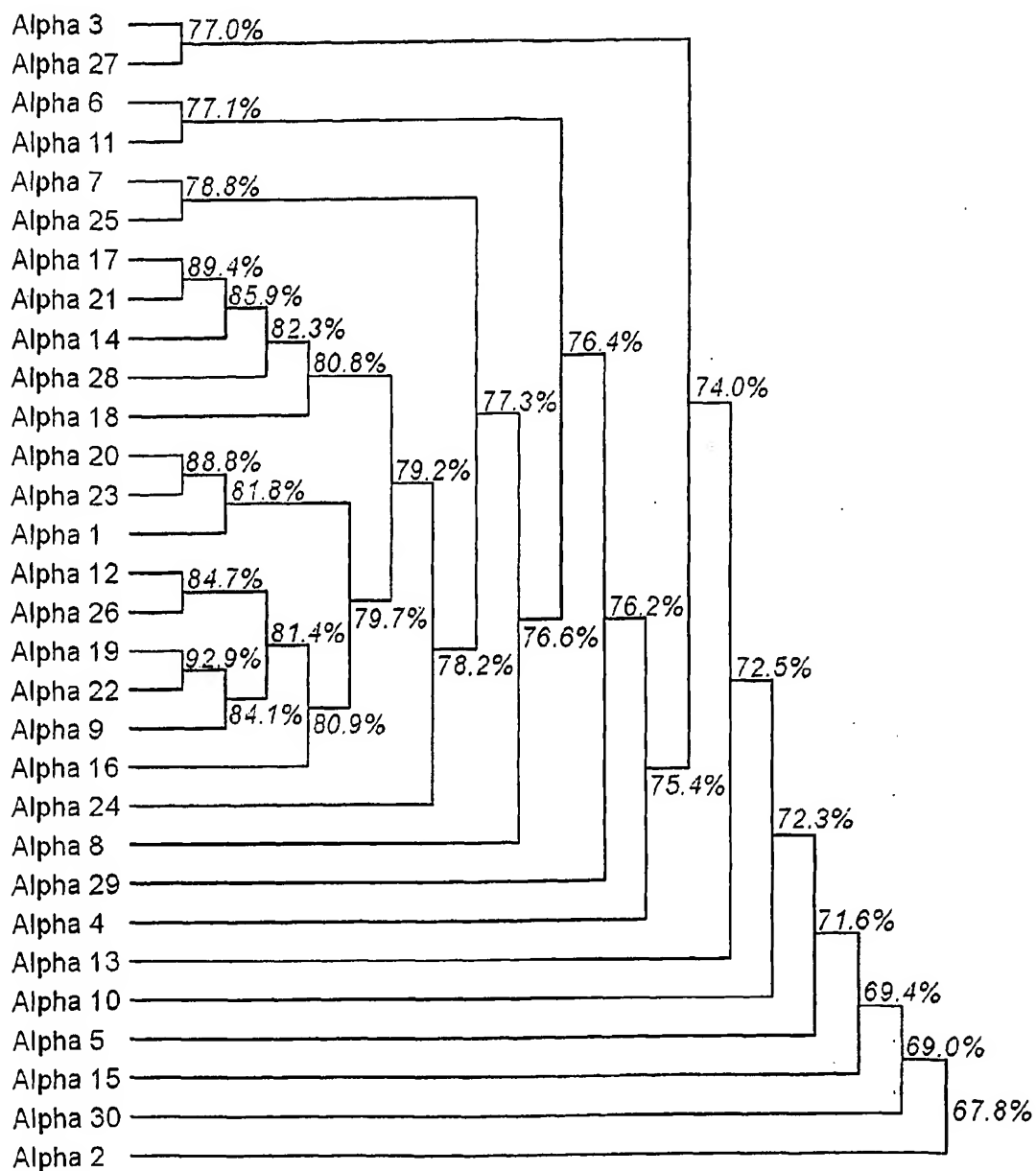


FIG. 5A

Phylogenetic tree of 28 alphaoid DNA repeats from chromosome 22

(Homology between repeats varies from 66% to 93%)

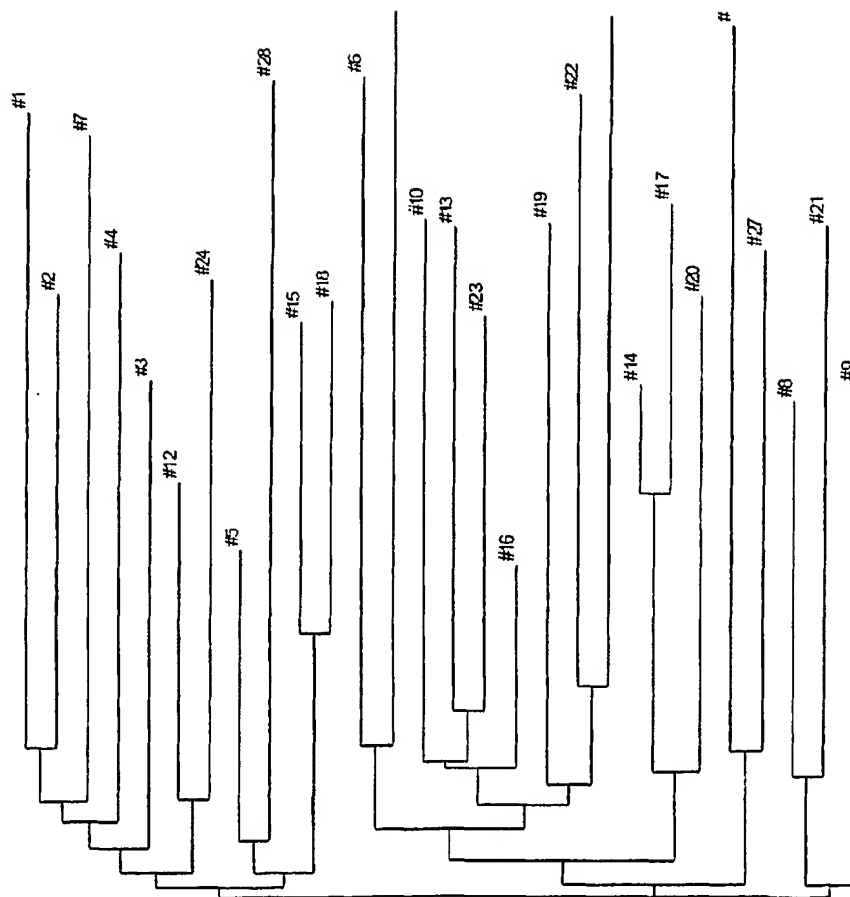


FIG. 5B

CCTGAGAGCAGGAAGAGCAAGATAAAAGGTAGTATTTGTTGGCGATCCCCCTAGAGTCTTTTACATCTTCGGAACCAAAACTAT
 TTTTTCTTAATTTCTTTTTTTTACTTTCTATTTTAAATTTATATATTATATTAATAATTTAAATTTATATTTTATATAGCAC
 GTGATGAAAAGGACCCCTAAGAAACCATTATATCATGACATTAACTATAAAAAATAGGCGTATCACGAGGCCCTTTCGTCTCGCGC
 GTTTCGGTGTATGACGGTGAAAACCTCTGACACATGCAGCTCCCGAGACGGTACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGA
 CAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCGGGTGTCCGGGCTGGCTTAACTATGCGGCATCAGASCAGATTGTACTGAGAGT
 GCACCATAATTCGGTTTTAAGAGCTTGGTGAGCGCTAGGAGTCACTGCCAGGTATCGTTTGAACACGGCATTAGTCAGGGAAGTCA
 TAACACAGTCCCTTTCCGCAATTTTCTTTTCTATTACTCTTGGCTCTCTAGTACACTCTATATTTTTTATGCTCGGTAAATG
 ATTTTCAATTTTTTTTTTTTCCACCTAGCGGATGACTCTTTTTTTTTCTTAGCGATTGGCATTATCACAATAATGAATTATACATTATA
 TAAAGTAATGTGATTTCTTCGAAGAATATACTAAAAAATGAGCAGGCAAGATAAACGAAGGCAAGATGACAGAGCAGAAAGCCCT
 AGTAAAGCGTATTACAAATGAACCAAGATTAGATTGCGATCTCTTTAAAGGGTGGTCCCTAGCGATAGAGCACTCGATCTTCC
 CAGAAAAAGAGGCAGAACGATGACAGAACAGGCCACACAATCGCAAGTGATTAACGTCCACACAGGTATAGGCTTTCGACCAT
 ATGATACATGCTCTGGCCAAAGCATTCGGCTGCTCGCTAATCGTTAGTGCATTGGTGACTTACACATAGACGACCATCACACCAC
 TGAAGACTGCGGGATTGCTCTCGGTCAAGCTTTTAAAGAGGCCCTACTGGCGGTGGAGTAAAAAGGTTTGGATCAGGATTGCGC
 CTTTGGATGAGGCACTTTCCAGAGCGGTGGTAGATCTTTCCGAACAGCCGTACGCAGTTTCCGAACCTGGTTTGCAGGAGGAGAA
 GTAGGAGATCTCTCTTGGCAGATGATCCCGCATTTCTTGAAAGCTTTGCGAGGGCTAGCAGAATTACCTCCACGTTGATTGTCT
 GCGAGGCAAGAATGATCATCACCGTAGTGAGAGTGCCTTCAAGGCTCTTGGGTTGCCATAAGAGAAGCCACCTCGCCCAATGGTA
 CCAACGATGTTCCCTCCACCAAGGTGTTCTTATGTAGTGACACGATTAATTTAAAGCTGCAGCATACGATATATACATATGTGTA
 TATATGTATACCTATGAATGTACAGTAAGTATGTATACGAACAGTATGATACTGAAGATGACAAAGGTAAATGATGATCGCCAACA
 ATACTACCTTTTATCTTGTCTCTCTGCTCTCAGGTATTAATGCCGAATTGTTTCATCTTGTCTGTGTAGAAGACCACACAGAAA
 ATCCTGTGATTTTACATTTTACTTTATCGTTAATCGAATGTATATCIAATTAATCTGCTTTCTTGTCTAATAAATATATATGTAAA
 GTACGCTTTTGTGTAATTTTAAACCTTTGTTTATTTTTTTTCTTCTATCCGTAACCTCTTCTACCTTCTTTATTTACTTTCT
 AAAATCCAAATACAAAACATAAAAAATAAATAAACACAGAGTAAATCCCAATATTCCATPCATTAAAGATACAGGCGGTGTA
 AGTTACAGGCAAGCGATCATCTATACGTGCTATTCTGAACGAGGCGCGCTTTCTTTTCTTTTGTCTTTTCTTTTCTTTTCT
 TTCTCTTGAACCTCGACGGATCATATGCGGTGTGAATAACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGAAATTGTAAACG
 TTAATATTTTGTAAAATTTCGCTTAAATTTTGTAAATCAGCTCAITTTTAAACCAATAGGCCGAAATCGGCAAAATCCGTTAT
 AAATCAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCAGTTTGAACAGAGTCCACTATTAAAGAAGCGTGGACTCCAACGT
 CAAAGGGCGAAAAACCTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCTTAATCAAGTTTGTGGGGTCGAGGTGCCGTA
 AAGCACTAAATCGGAACCTTAAAGGAGCGCCCGATTTAGAGCTTGAAGGGGAAAGCGCGCAACGTGGCGAGAAAGGAAGGAAG
 AAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCAAGCTGCGCGTAACCAACACACCCGCGCGCTTAATGCGCC
 GCTACAGGGCGCGCTGCGCCATTGCGCCATTAGGCTGCGCACTGTGGGAAGGGCGATCGGTGCGGGCTCTTCTGCTATTACGCC
 AGCTGCGGAAGGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAAAGCCAGGGTTTCCAGTCAAGAGCTGTAAAACGAGCGCC
 AGTGAATTTGAATACGACTACATAGGGCGAATTGGAGCTCCACCGCGGCAATCTCAGAACTTCTTTGTGATGTGTGCATTCAA
 CTCACAGAGTTGAACCTTCCTTTGGATCCATATTTAAATATTGAPAGCTGCAAGATTTAAAAAATCTCCGGGGGCGAGTCCGA
 CGCCGATCTCAAGATTTCTAGTGGTAAATTACAGTCTTGGGCTTAAACCACTTGGCTACCGAGAGTCTGTTTGTGTGTA
 CAGGATCGATAAAGGAAGGTTCAACTCTGTGAGTTGAATGCACACATCACAAAGAGTTTCTGAGAATGGGGCGGTACCCAG
 CTTTGTCTCCCTTTAGTGAGGTTAATTCGAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAATTTGTATCCGCTCA
 CAATTCACACAACATAGGAGCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGGTAACTCACATTAATTCGGTTG
 CGCTCACTGCGCGCTTTCCAGTCSGGAAACCTGTCTGTCAGCTGCATTAATGAATCGGCCAACGCGGGGAGAGGCGGTTTGGC
 TATTGGGCGCTCTTCCGCTTCTCTGCTCACTGACTCGCTGCGCTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGG
 CGGTAATACGGTTATCCACGAPATCAGGGGATAACCGAGGAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAA
 AAGCCGCGCTTGGCTGGCGTTTTTCTATAGGCTCGGCCCCCTGACGAGCATCACAATAATCGACGCTCAAGTCAGAGGTGGCGAAA
 CCCGACAGGACTATAAGATACAGGCGTTCCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCCTGCGCTTACCGGAT
 ACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTCTGTCG
 TCCAAGCTGGGCTGTGTGCACGAACCCCGCTTACGCGCGACCGCTGCGCTTATCCGGTAACATATCGTCTTGAGTCCACCCGGT
 AAGACACGACTTATCGCCAC TGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTACAGAGTTCTTGA
 AGTGGTGGCTAACTACGGCTACACTAGAAGACAGTATTTGGTATCTGCGCTCTGCTGAAGCGAGTTACCTTCGGAAGAAAGAGTT
 GGTAGCTCTTGATCCGGCAACAAACACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGG
 ATCTCAAGAAGATCTTTGATCTTTTCTACGGGCTGTGACGCTCAGTGAACGAAACTCACGTTAAGGGATTTTGGTCAATGAGAT
 TATCAAAAAGGATCTTCACTAGATCTTTTAAATTAATAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAACTTGGTCT
 GACAGTTACCAATGCTTAATCAGTGAGGCACTATCTCAGCGATCTGTCTATTTCTGTTTATCCATAGTTTGGCTGACTGCCCGTCT
 GTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGGAGACCCAGCTCACCGGCTCCAGATT
 TATCAGCAATAAACCGACGAGCCGGAAGGGCCGAGCGCAGAAAGTGGTCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTGT
 TGCCGGGAAGCTAGAGTAAGTAGTTCCGCCAGTTAATAGTTTGGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACGCTC
 GTCGTTTGGTATGGCTTCAATCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCATGTTGTGAAAAAAGCGGTTA
 GCTCCTTCGGTCTCCGATCCTGTGTCAGAAAGTGTGGCCGAGTGTATCACTCATGTTTATGGCAGCTGCATAATTCTCTT
 ACTGTATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAAGTACTCAACCAAGTCACTTGTGAGAAATGTTATGCGGCGACCGAG
 TTGCTCTTGGCCGCGCTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAGTGTCTCATTTGGAAACCTCTTCGG
 GCGGAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTACACCACTCGTGACCCCACTGATCTTCAAGCATCTTTT
 ACTTTACACAGCTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAGGCGACACGGAATGTTGAAT
 ACTCATACTCTTCTTTTCAATATTTATGAAGCATTTATCAGGTTTATGTCTCATGAGCGGATACATATTTGAATGTATTTAGA
 AAAATAAACAAATAGGGGTTCCGCGCACATTTCCCGGAAAGTGCCACCTGGACGGATCGCTTGCCGTAACTTACACGCGCTCG
 TAGG

FIG 6

2.9 kb Spel fragment

ACTAGTCAATCAAAGAAAGGTTCAACTCTGTCAGTTGAATGCACATATCACAAACAAGTTTCTC
GGAATGCGTCTGTGTAGTTTTTATGTGAAGATATTTCTTCTCCACAACAGGCCTCAAAGTGCTC
CGAATATCCACTTGCAGATTTTACTAAAGAGTGTTCCAAAGTCTCAATCAAGAGGAAGTTTCA
AGTCTGTGAGCTGAACGCACACATCACAAAGTAGTTTCTGAGAATGCTTCTGTGTAGTTTTTATG
TGAAGATGTTTTCTTTTCCACCATAGGCTGCAAAGGGCTCCAAATATCCACTTGCAGATTCTACA
AAAAGAGAGTTTTCAAAGTGCTCTATCAAAGATAGGTTCAACTATGTGATATGAATGCACACAT
CACAAAGTAGTTTTCTCAGAATGCTTCTGTGTAGTTTTTATGTAAAGATATTTCTTTTTCCACCAT
AGGCCTCAAAGCACTCCAAATATCCACTTGCAGATTCTACAAAAGAGATTTTCAAAGTATTTA
ATCAAAGAAAGGTTCAATCTGTCAGTTGAAGGTACATATCACAAACAAGTTTATTGGAATGCT
TCTGTGTAGTTTTTATGTGAAGATATTTCTTTTTCCACAACAGGCCTCAAGGTGCTCCAAATATC
CACTTGCAGATTTCACTAAAAGTGTGTTTCCAAGCTGCTCAATCAAGAGGAAGTTTCAAGTCTGT
GAGGTGAATGCACACATTACAAAGAAGTTACTGAGAATGCTTCTGTGTAGTTTATGTGAAGAT
ATTTCTTTTTCCACCGCAGGCCTCAAAGCGCTGCAATATCCACTTGCAGATTCTACAAAAGAG
AGTTTCAAAGTGTGTATCAAAGATAGGTTCAACTCTGCGAGTTGAATAAGCACATCACAAAT
AAGTTTCTGGGAACGCTTCTGTATAGTTTTTATGTGAATATATTTCTTTTTCCACCATATGCCTCA
AAGCACTCCAAATATCCACTTGCACATTATAGAAACATAGTCTTTCAAAGTCTCAATCAAAGA
AAGGTTCAACTCCGTGAGATGAGTGCACACATCACAGAGAAGTTTCTCGGAATGTTTCTGTGTAG
TTTTTATGTGAAGATATTGCTTTTTCCACAATAGGCCTCAAAGCGTTCCAAATATCCAATTGCAG
ATTCCACAAAAAAGTTTTTTAAAGTGTCTCAATCAAATGATAGATTAAAGTCTGTGAGATTAGT
GCACACATGTCAAAAAAGTTTTCTCAGAATGCTTCTGTGTACTTTTTAGGGGAAGATATTTCTTTT
TCCACCATCGGCCACAAAGGACTCCAAATAACCACATGCAGATTCTAGTAACACAGAGTTTCAAA
ACTGCTCTATCAAAGATAAGTTCAACTCTGAGAGTTTAGTGCAACCATCGTGAAGAAGTTTCTC
AGAATGCTTCTGAGTAGTGTATGTGAAGATATTTCTTTTTCCACCATAGGCCTGAAAGCCCTC
CAAATATCCACTTGCAGATCCTACAAAAGAAAGTTTTCGAAATGCTCTCTCAAACGATAGTTTCG
ACTCTGTGGTATGAATACACACATCACAAAGAAGTTTCTCAGAATGCTTCTGTGTAGTTTTTAA
TGAAGATATTTCTTTTTCCACCATAGGCCTCAAAGCACTCCAAATATGCACTTCCAGATTCTACA
AAAAGAGTGTTCAGAAGTGTCAATCAAAGGAAGGTTCCAGTCTGAGACAAATACACACATCA
AAAGGTAGTTTCTCAGAATGCTTCTGTGTAGTTTTTATGTGAAGATATTTCTTTTTCCACCATAG
GCCACAAATGGCTCTAAATACCCACTTACATTTTCCACAAAAAGAGAGTTTCAAAGTGTCTAC
CAAAGGTAAGTTTAAAGCTGTGAGTTAAGAACATCACAAAGAAGTTTCTCAGAATGCTTCTGTGT
AGTTCTTACGTAAAGATATTTCTTTTTACACAATAGGCAGAAAAGTGCTCCAAATATCCACTTGA
AGATTCTACAGAAACCGTGTTCCAAAGTGTCCGAATCAAAGAAAGGTTCAACTCTGTGAGATGA
ATGCACACATAACAAAGGAGTTTCTCAGAATGCTTCTGTGTAGCTTTTATATGAAGACATTTAGT
TTTCCACAACAGGCCTCAAAGCTCTCTCCATATCCACTTGCAGATTCTACCGAAAGAGTGCTTCC
AAAGTGTCAATCAAAGSAGACATTCAAATCTGTGAGGTGAATGCAGACATCGTAAGAAGTTTC
TCAGAATGCTTCTGTGTATTTTTTGTGTGAAGTTATTCGTTTTTGCACCATAGGCCTCCAAGCGT
TCTAAATATCCACTTCTAGATTCTACAAAAGAGAGTTTCAAAGTACTCAAACAAAAGGTTCAA
TTCTGTGAGTTGAAGCAAACATCACAAAGAAGTTTCTCAGAATGCGTCTGTGTAGTTTTGATGT
GAAGATATTTCTTTTTACAGTAGAATGCAAAGGGCTCCAAATATCCACTTGGAGATTCTACAAA
AAGAGTTTCAAACCGCTCTGTCAAATGATAGGTTGAACTCCCGGAGGTGAATACACACATCACA
AAGAGGTTTCTCAGCATGCTTCTGTGTAGTTTTTATGTAAACATATTTCCGTTTCTATCATAGGC
CTCAAAGTGTCTCAAATATTCATTGTACATTCTACCAAAGAGTATTTCAAAGTGTCTCAATCA
AATGGAAGGTTCAAACCGTGACATGAATGCCACATCACAAAGTAGTTTCTCAGAATGCTTCTGT
TGAGTTTTTATGTGAAGATATTTCTTTTTCCACAACAGCGTGCAAACGCTTCAAATATGCCCT
TAGAGATTCCACAAAAAGAGTGTTCCAAAGTACTCAAATCAAAAAATGATTCAACTCTGTGAG
ATGAATGCACACATCACAAAGTAGT

FIG 7

2.8 kb *SpeI* fragment

ACTAGTTTCTCAGAATGTTTCTGCCTGGTTCTCATGCGAAGATAGTTCTTTTTCACCATAGGCC
GCAATGTACTCCAAATATCCACCTGCAGATTCTACAAAAGTGAGTTTCAAACCTGCTCTATCAAA
AGATCAGTTCGTCTCTGTGAGTTGAATGCATACATCAAAAAGAAGCTTCTCAAATGCTTCTGTG
TGGTTTTTTCGGTGAAGATAGTTCTTTTTCTACCATAGGTCTCAAACCACTCCAAATATCCACTTG
TAGATTCTATAAAAAGGAATGTTCAAATGCTCAATAAAAATAAAGTTTCAACACCGTGAGATG
AGTGCACAAATCACAAAGGAGTTTCTCAAATGCTTCTGGGTAGTTTTTCTGTGAAGATAGTTCC
TTTTCTACCATGGGCCACAAAGGGCTCCAAATACCCACTTGCGAGATTCTACAAAAGAGAGTTTC
ACAACTGCTCTATCAAACAATATGTTCAACTTTGTGGGTGAACACAAATATCACAGAATTTTTC
TCCCAATGCTTCTGTGTAGTTTTTATGTGAAGACATTTCTTTTCCCTCCATAGTCCACAAAGTGC
TCCAAATATCCACTTACATATTCTAGAAAAAGATTGCTTGGAACTGCACAATGAAAAGAAAGGT
TCAAATATATGAGATGAATGCACACATCACAAAGAAGTTTCTCAGAATCTCTCTGTGTAATTTTT
ATGTGAAGATATTTCTTTCCACCTTAGGTCTTAAACGCTCCAAATATCCACTTGCGAGATACT
ACAAGAAGATTGTTTCAAACCTGCACAAAAAAGAAATGTTCAATTCTGTTTGATGAATGCACAC
ATCACAAAGAAGTTTCTCAGAATGCTTCTCTGTAGTTTTTATGTGAAGATATTTCTTTTCCACA
ATAGGCCTCAAAGGGCTCCAAATATCCACTTCCAGATTCTATGAAAAGAATATTTCCAACTGCT
CAATCATAGGAAATGTTCAACTCTGTGAGATGAATGCACACATCACAAAGAAATTTCTCAGAATCC
TTCAGTGTAGGTTTTATGAGAAGATAATTCTTTTCCACAATAGTTCTCAAAGCACTCAAATAT
CCACTTGCGAGATTCTACAAAAGGAGTATTTCAAACCTGCTCAATCAAAGAAAGGTTCAACTCTG
TGAGATGAATGGACACATCACAAAGAAGTTTCTCAGAATGCTTCTGTGTAGTATTTTGTGAAGA
TATTTCTTTTCCACCATAGACCGCCAGGGGACACAAATATCCACTTTCAGATTCTACAACAAGAG
AGGTTCAAACCTACTCGATCAAGAGATGGTTTCAACTATGTGAGTTGAATGCACACATCACAAAG
AACTATGTGGAATTCTTCTGTGTAGTTTTTATGTGAAGATATTTCTTTTCCACAATAGACGTC
AAAGTGATCCAGATATCCACTTGCGAGATTCCACAAAAGAGTGTTTCAAAGTGCGACAACCAAAA
GAAAGGTTCAACTAGGTGAGATGAATGCACACATCAGAAGGAAGTTTCTCAGAATGCTTCTGCGAT
AGCTTTTAAAGGAAGATACTTCTTTTCCACATAGGCCTCAAAGCACTCCAAATATCCTCCTGG
AGATACCACAAAAGAGTGTTTGCAAACCTGCTCAATCAAAGAAAGATTTAACTCTGTGAGATGA
ATCCACACATGACAAAGAAGTTTCTCAGAATGCTTCTGTGTAGTTTTTATGTGAAGATATTTCT
TTTCCACAATAAGACCCAAAAGGCTCCAAATATTCACTTGCGAGATTCTAAAAAAACAGTGTTTC
AAAACCTGCTCAATCAAAGATAGTTCAACTCTGTGAGAAGATGCTCACATCACTGAGAAGTTTC
TCAGAATGCTTCTGTGTAGTTTTTATATGAAGATATTTCTTTCCACCGTAGGCCACAAAAGGC
TCCAAATATCCACTTGCGAGATACTATGAAAAGAGAGTTTCAAACCTGCTCATTCAAAGATAGGT
TCAACTCTGTGGTTTGAATGCACACAGCACAAAGAAGTTTCAAGAATGTGTCTGTGTAGTTTTT
ATGTGCGGATGTTTCTTTTCCACCATATGCCTAAATATTTCCCAATTTCCACTTGCGAGATTCTA
CAAGAAGAGTGTTTCAAACCTGCTGTATCAAATAAAGTTGAACTCTGTGAGGTGAATGCACACAG
CACAAATGGTTTCTCAGAATGCTTCTTGTGTTTTTATATGAAGATGTTTCTTTTCAACAAT
AGGCCTCAAAGTGCTTCAAATGTCCACTTGCGAGATTCTACAAAAGAGTGTTTCAAACCTGCTCA
ATCAAAGAAAGGTTGCGACTCTGGGAAATTAATGCACACATCACAAAGAAGTTTCTCAGCTTCTG
TGTAGTTTTTCATGTGAAGTTATTTCTTTTCCACAATAGGCCGCAAAGGGCTCCAAATATCAACT
TACAGATTCTAGGAAAAGAGAGTTTCAAACCTGCTCTACGAAAAGATAGGTGAACTCTGTGAGA
TGAATGCACACATCACAAAGAAGTTTCTCAGAATGCATCTGTGTAGTTTTTACGGGAAGACATTT
CCTTTTCCACCATCTTCCACAAAGGTCTCAAGTAACCACTTGCGAGATTCTACAGAAAGACACTT
TAAAACTGCTCTATCAAAGATCAGTTCAAGTCTGTGGTTTGAATGCACACATCACAAAGAATT
TTCTCAGAATGCTTCTGTGTAGTTTTCATATGAAGATATTTCTTTTCCACCATAGGCCTCAAAG
CACTCCAAATATCCACTTGCGAGATTCTACAAAAGAGATTTTCAAACCTAGT

FIG 8

		10	20	30	40	50	
Stu0.17A	1	CCTCAAAGCC	CTCCAAATAT	CCACTTGCAG	ATCCTACAAA	AAGAGATT	50
Stu0.17B	1	CCTCAAAGCA	CTCCAAATAT	CCACTTGCAG	ATTCTACAAA	AAGAGATT	50
Stu0.17C	1	CCTCAAAGGT	CTCTCCATAT	CCACTTGCAG	ATTCTACCGA	AAGAGTGC	50
Stu0.17D	1	CCTCAAAGCA	CTCCAAATAT	CCACTTGCAG	ATTCTACAAA	AAGAGATT	50
STU0.17E	1	CCTCAAAGTG	CTCCAAATAT	CCACTTGCAG	ATTCTACTAA	AAGTGTGTT	50
		60	70	80	90	100	
Stu0.17A	51	CGAAA-TCCT	CTCTCAAACG	ATAGTTTGG	CTCTGTGCTA	TGAATACACA	100
Stu0.17B	51	CGAAACTATT	TAATCAAAAG	AAAGGTTCAA	ATCTGTCACT	TGAAGGTACA	100
Stu0.17C	51	CGAAACTGCT	CAATCAAAAG	AGACATTCAA	ATCTGTGAGG	TGAATGCACA	100
Stu0.17D	51	CGAAACTAGT	CAATCAAAAG	AAAGGTTCAA	CTCTGTCACT	TGAATGCACA	100
STU0.17E	51	CGAAGCTGCT	CAATCAAGAG	GAAGTTTCAA	GTCTGTGAGG	TGAATGCACA	100
		SpeI					
		110	120	130	140	150	
Stu0.17A	101	CATCACAAC	AAGTTTCTGA	GAATGCTTCT	GTGTAGTTTT	TAAATGAAGA	150
Stu0.17B	101	TATCACAAC	AAGTTTATFG	GAATGCTTCT	GTGTAGTTTT	TATGTGAAGA	150
Stu0.17C	101	CATCGTAAAG	AAGTTTCTGA	GAATGCTTCT	GTGTATTTTT	TGTGTERAGT	150
Stu0.17D	101	TATCACAAC	AAGTTTCTGG	GAATGCTTCT	GTGTAGTTTT	TATGTGAAGA	150
STU0.17E	101	CATTACAAAG	AAGTTTCTGA	GAATGCTTCT	GTGTAGTTTT	TATGTGAAGA	150
		160	170	180	190	200	
Stu0.17A	151	TATTTCTTTT	TCCACCATAG	G.....	200
Stu0.17B	151	TATTTCTTTT	TCCACCATAG	G.....	200
Stu0.17C	151	TATTTCTTTT	TCCACCATAG	G.....	200
Stu0.17D	151	TATTTCTTTT	TCCACCATAG	G.....	200
STU0.17E	151	TATTTCTTTT	TCCACCATAG	G.....	200

FIG. 9A

		10	20	30	40	50	
Stu0.34A	1	CCTCAAAGCG	CTGCAAAATAT	CCAGTTGCAG	ATTCTACAAA	AAGAGAGTTT	50
Stu0.34B	1	CCTCAAAGCG	TTGCAAAATAT	CCAAATTGCAG	ATTCCACAAA	AAAAGTITTT	50
Stu0.34C	1	CCTCAAAGTG	CTCCGAATAT	CCACTTGCAG	ATTTTACTAA	ACA-GTGTIT	50
Stu0.34D	1	CCTCAAAGCG	TTCTAAATAT	CCACTTCTAG	ATTCTACAAA	AAGAGAGTTT	50
		60	70	80	90	100	
Stu0.34A	51	CAAAACTGCT	GATCAAAAG	ATAGGTCZA	CTCTGCGAGT	TGAATAAGCA	100
Stu0.34B	51	TAAAACTGCT	CAATCAAAATG	ATAGATTAA	CTCTGTGAGA	TTAGTGCAGA	100
Stu0.34C	51	CCAAACTGCT	CAATCAAGAG	GAAGTTTCAA	CTCTGTGAGC	TGAACGCAGA	100
Stu0.34D	51	CAAACTACT	CAACAA--	AGTTTCAA	TTCTGTGAGT	TGAAGCCAA	100
		110	120	130	140	150	
Stu0.34A	101	CATCACAAT	AAGTTTCTGG	GAACGCTTCT	GTAATAGTTT	-ATGTGAATA	150
Stu0.34B	101	CATGTCAAA	AAGTTTCTGA	GAATGCTTCT	GTCTACTTTT	TTAGGGCAAGA	150
Stu0.34C	101	CATCACAAG	TAGTTTCTGA	GAATGCTTCT	GTCTAGTTT	TTATGTGAAGA	150
Stu0.34D	101	CATCACAAG	AAGTTTCTGA	GAATGCTTCT	GTCTAGTTT	CATGTCGAAGA	150
		160	170	180	190	200	
Stu0.34A	151	TATTTCTT	TCCACATAT	GCTCAAAAGC	ACTCCAAATA	TCCACTTCCA	200
Stu0.34B	151	TATTTCTT	TCCACCATCG	GCCAGAAAGC	ACTCCAAATA	ACCAGATCCA	200
Stu0.34C	151	TATTTCTT	TCCACCATAG	GCTCAAAAGC	GCTCCAAATA	TCCACTTCCA	200
Stu0.34D	151	TATTTCTT	TC-ACACTAG	AATGCAAGC	GCTCCAAATA	TCCACTTCCA	200
		210	220	230	240	250	
Stu0.34A	201	CATTATAGAA	ACATAGTCTT	TCAAAACTTG	TCAATCAAAG	AA-AGGTTCA	250
Stu0.34B	201	CATTGTAGTA	ACACAGAGTT	TCAAAACTTG	TCTATCAAAA	CATTAAGTTCA	250
Stu0.34C	201	CATTCTAGAA	AAAGAGAGTT	TCAAAACTTG	TCTATCAAAA	CATTAGGTTCA	250
Stu0.34D	201	CATTCTAGAA	AAA--GAGTT	TCAAAACCGC	TCTGTCAAT	CATTAGGTTCA	250
		260	270	280	290	300	
Stu0.34A	251	AGTCCGTCAG	ATGACTGCAG	ACATCAGACA	GAGGTTTCTC	GGAATGTTTC	300
Stu0.34B	251	AGTCTCAGAG	TTTACTGCCAA	CCATCGTGAA	GAGGTTTCTC	AAATGCTTTC	300
Stu0.34C	251	AGTATGATAT	ATGAATGCAG	ACATCAGAAA	GAGGTTTCTC	AAATGCTTTC	300
Stu0.34D	251	AGTCCCGAG	GTGAATACAG	ACATCAGAAA	GAGGTTTCTC	ACATGCTTTC	300
		310	320	330	340	350	
Stu0.34A	301	TGTGTAGTTT	TTATGTAAAG	ATATTCGCTT	TTCCACAATA	GC.....	350
Stu0.34B	301	TGAGTAGTTT	TTATGTAAAG	ATATTCGCTT	TTCCACCATA	GC.....	350
Stu0.34C	301	TGTGTAGTTT	TTATGTAAAG	ATATTCGCTT	TTCCACCATA	GC.....	350
Stu0.34D	301	TGTGTAGTTT	TTATGTAAAG	ATATTCGCTT	TTCTATCAATA	GC.....	350

FIG. 9B

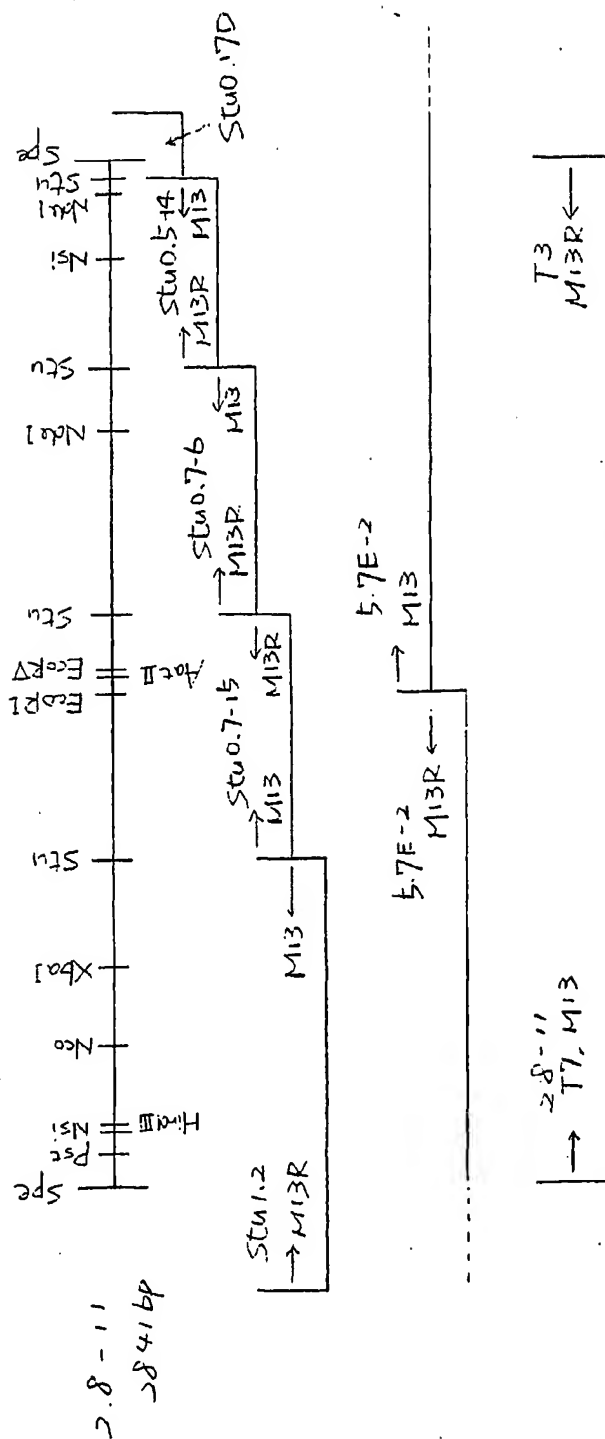


FIG. 10

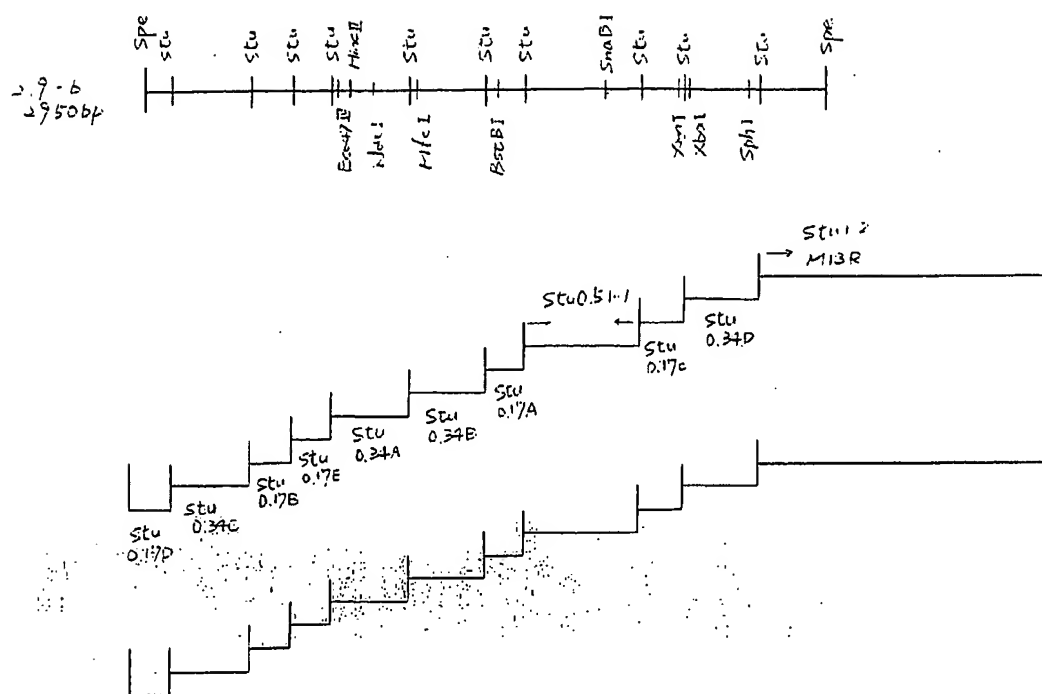


FIG. 11

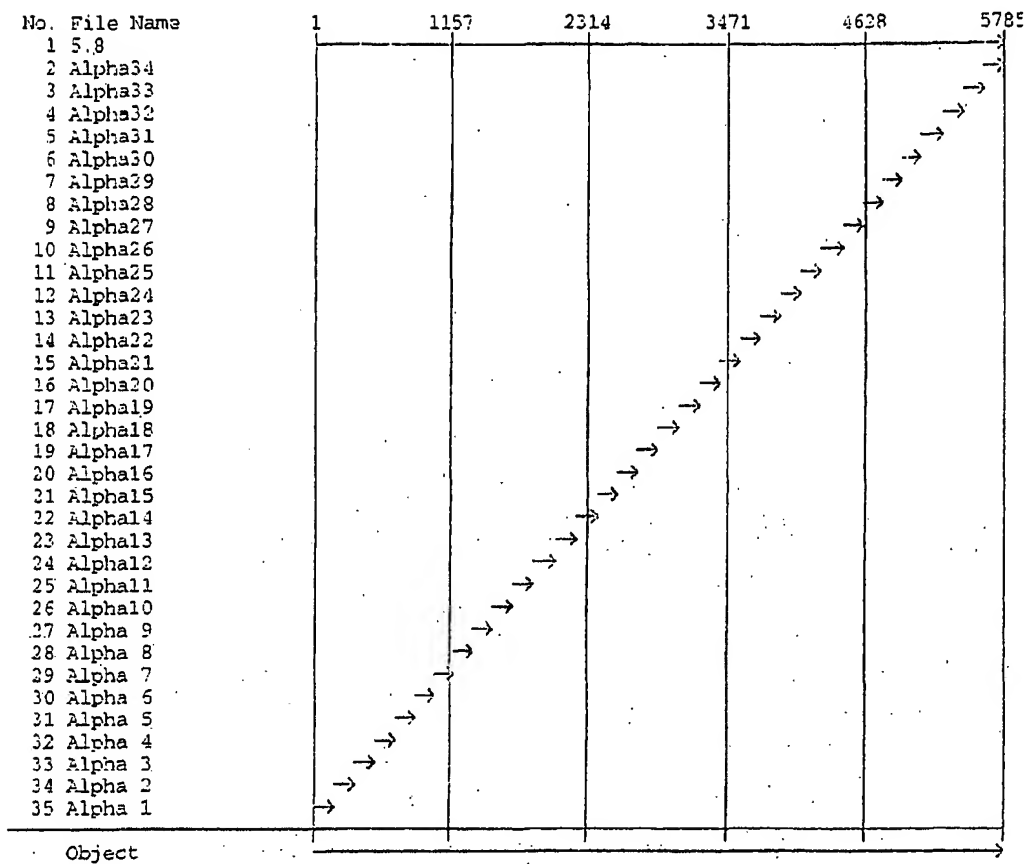


FIG. 12

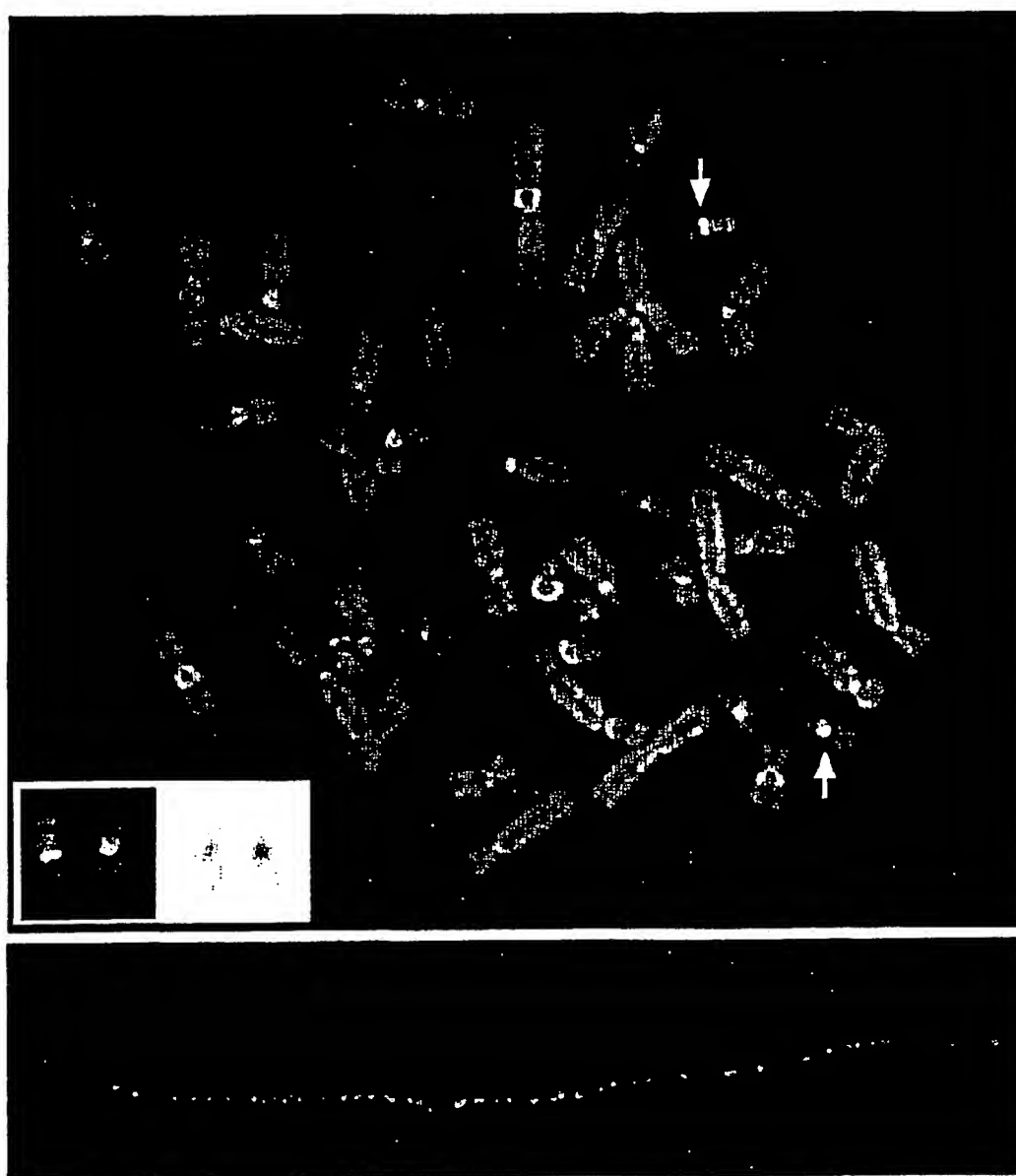
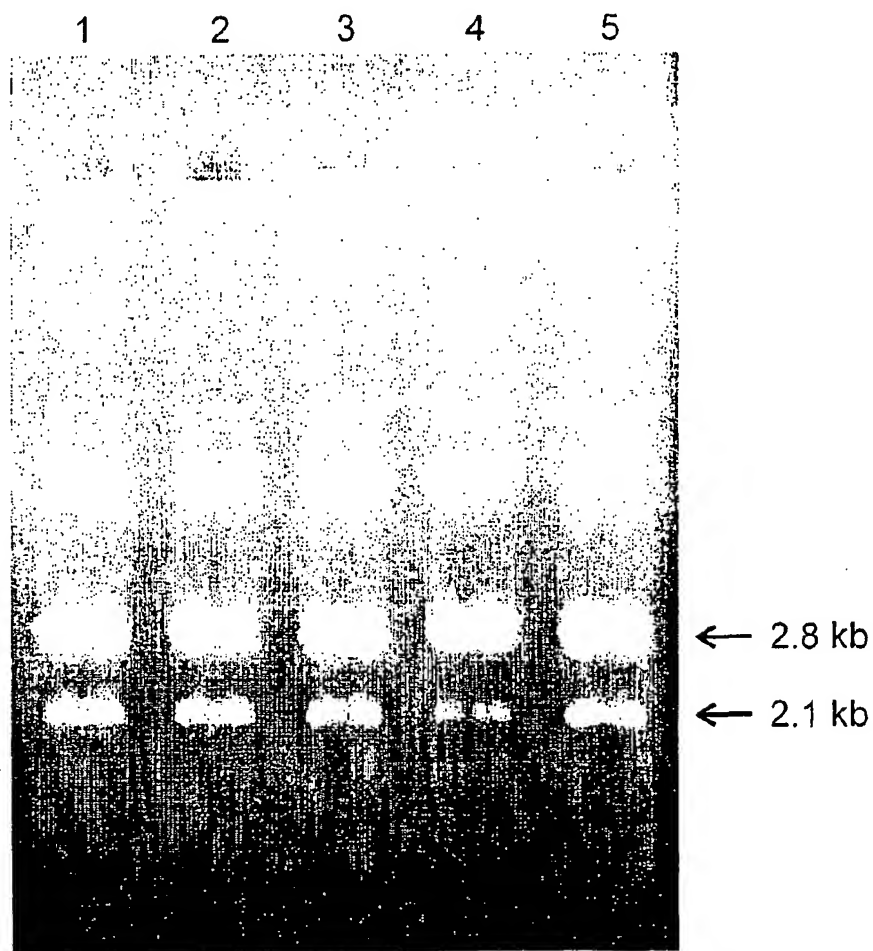


FIG. 13

EcoRI digestion of BAC/YACs containing alphoid DNA repeats from human chromosome 22



1, 2 - 100 kb inserts
3 - 140 kb insert
4 - 70 kb insert
5 - 160 kb insert

FIG. 14



FIG. 15

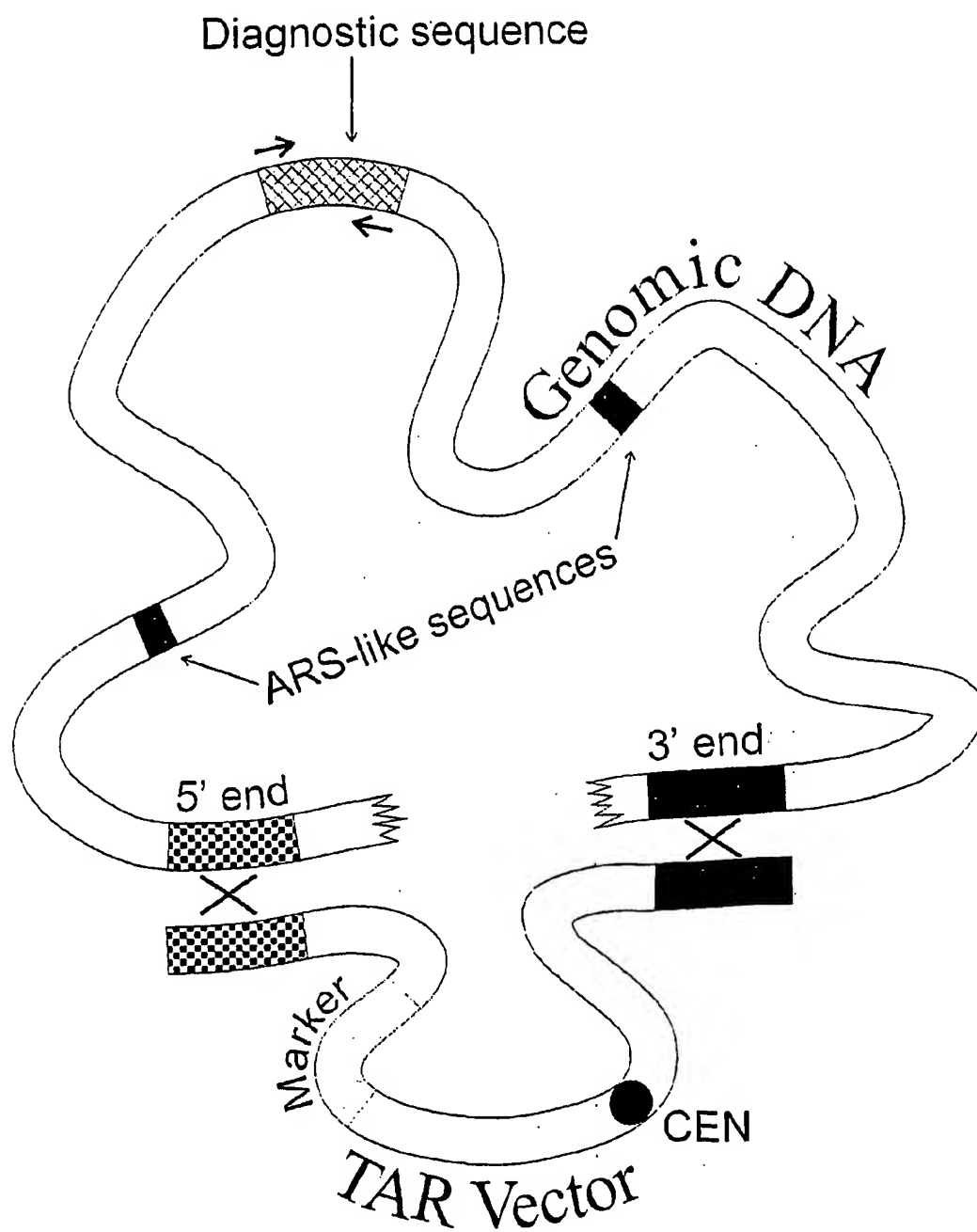
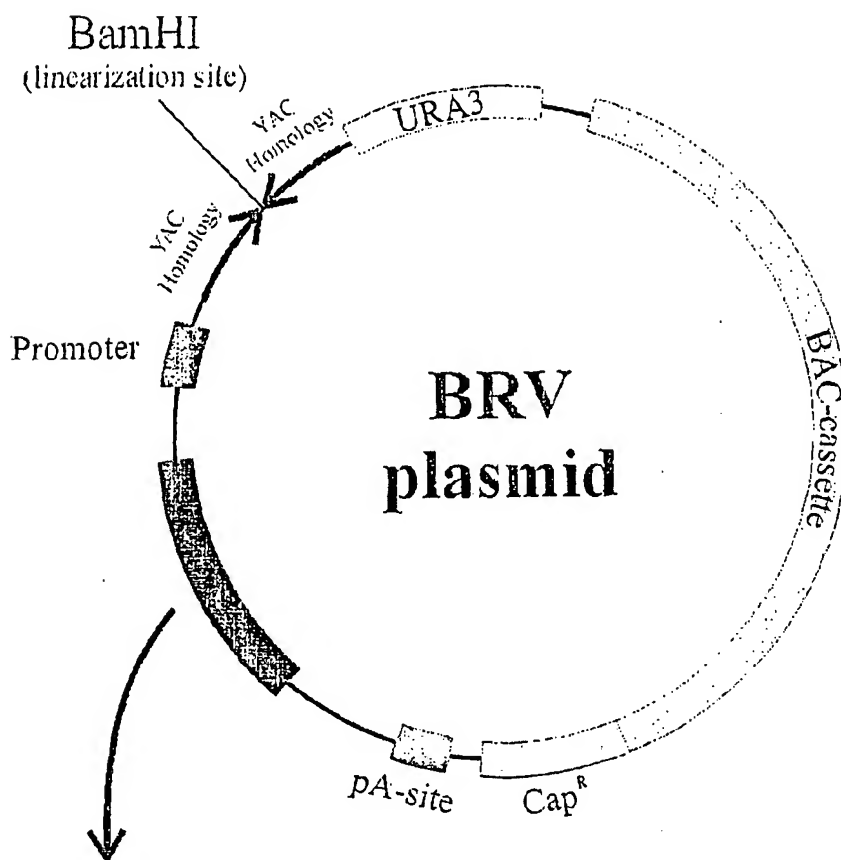


FIG. 16

BAC Retrofitting Vectors (BRV)



Marker for selection in mammalian cells

- | |
|--|
| <p>BRV-N - Neomycin phosphotransferase (Neo)</p> <p>BRV-B - Blasticidin-S-deaminase (Bsd)</p> <p>BRV-H - Hygromycin phosphotransferase (Hyg)</p> <p>BRV-C - Hyg-CodA (Cytosine deaminase) fusion</p> |
|--|

FIG 17

Organization of Main Alphoid DNA Array in Centromere Region of Chromosome 13

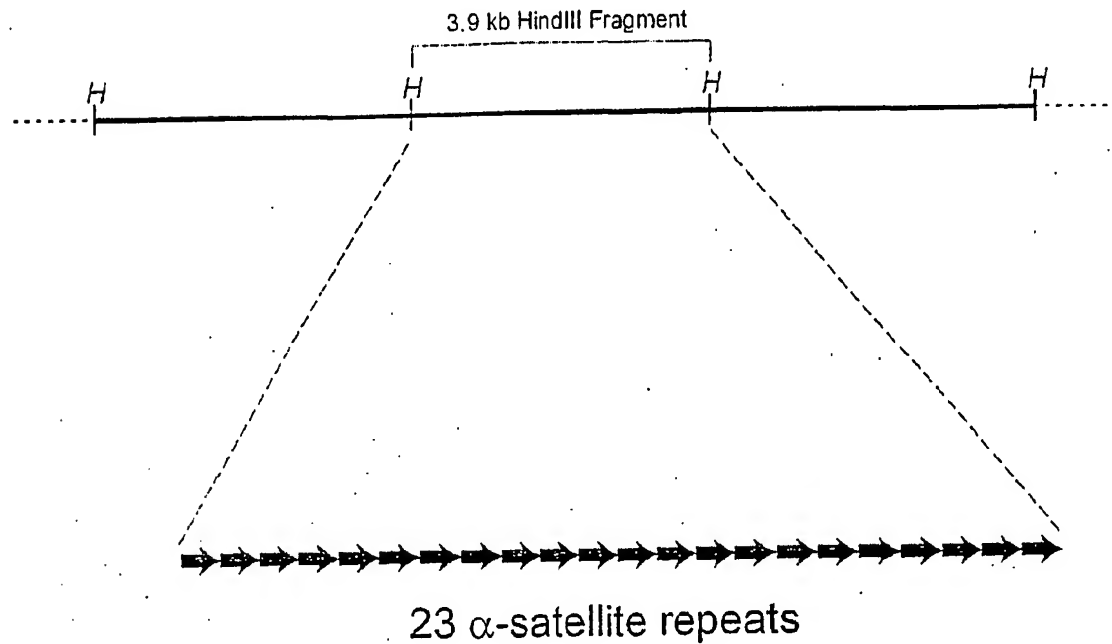


FIG. 18

***Organization of Main Alphoid DNA Array
in Centromere Region of Chromosome 22***

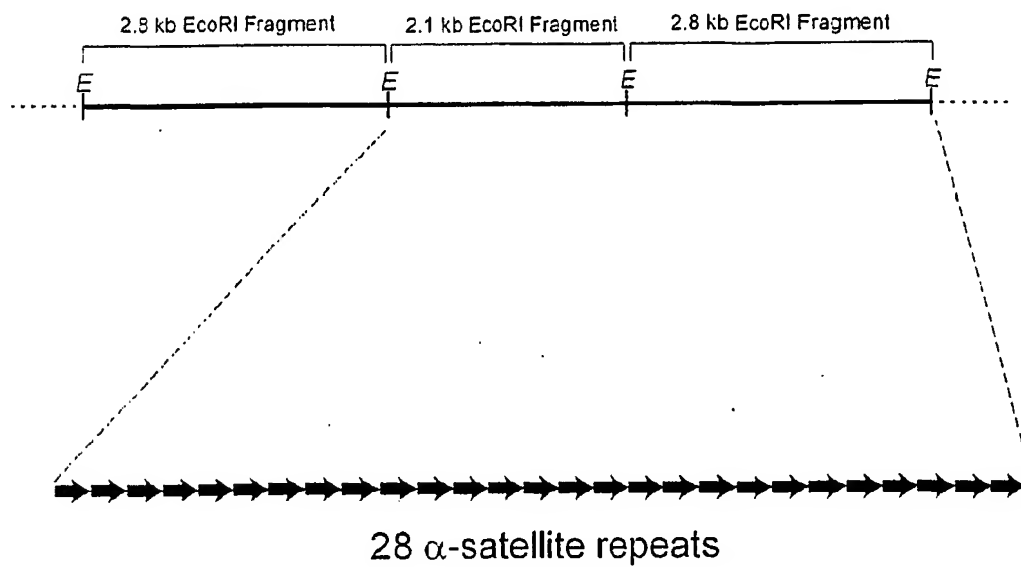


FIG. 19

EcoRI Digestion of BAC Clones Containing Centromeric Regions from Chromosome 22

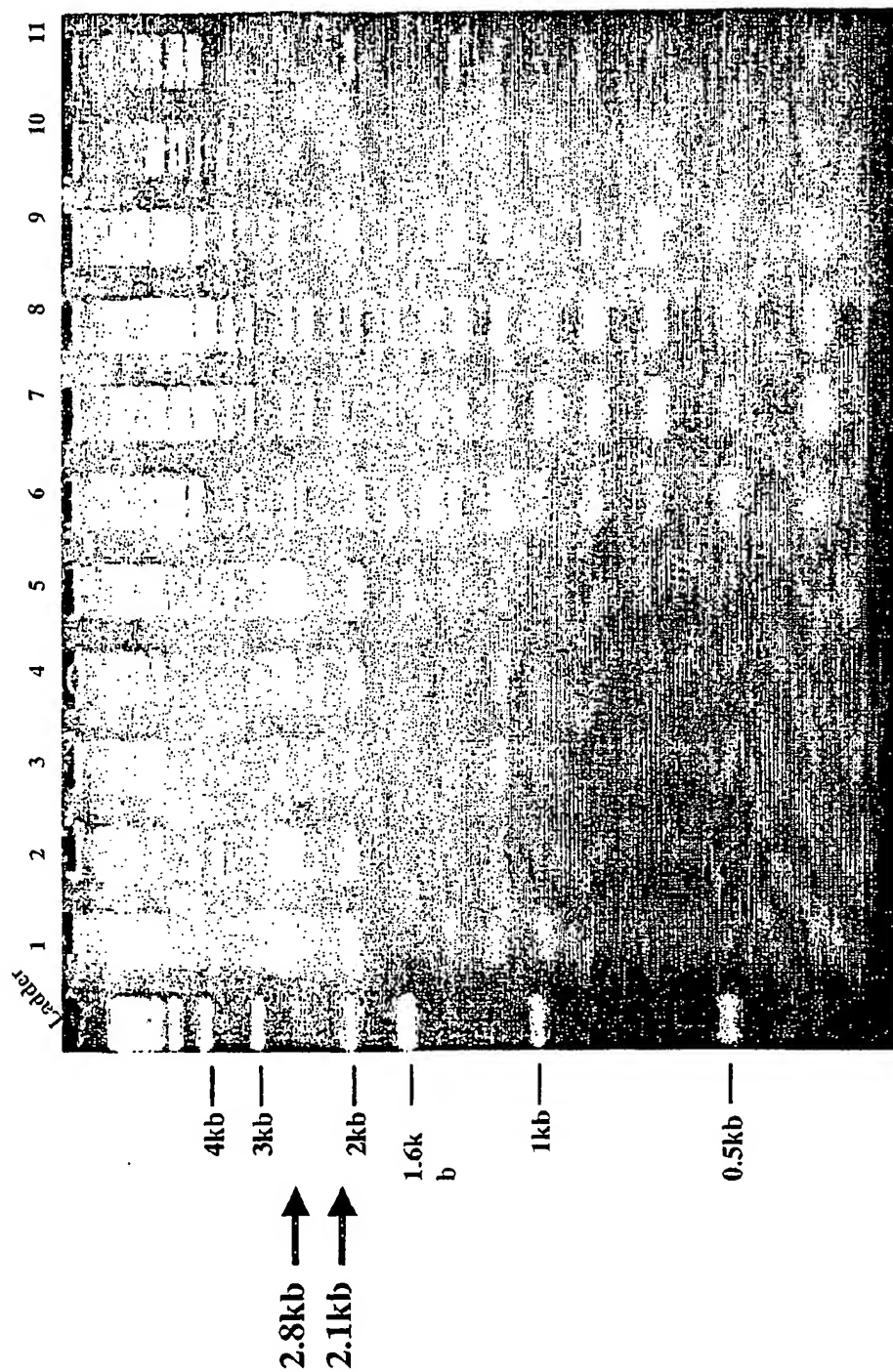


FIG. 20

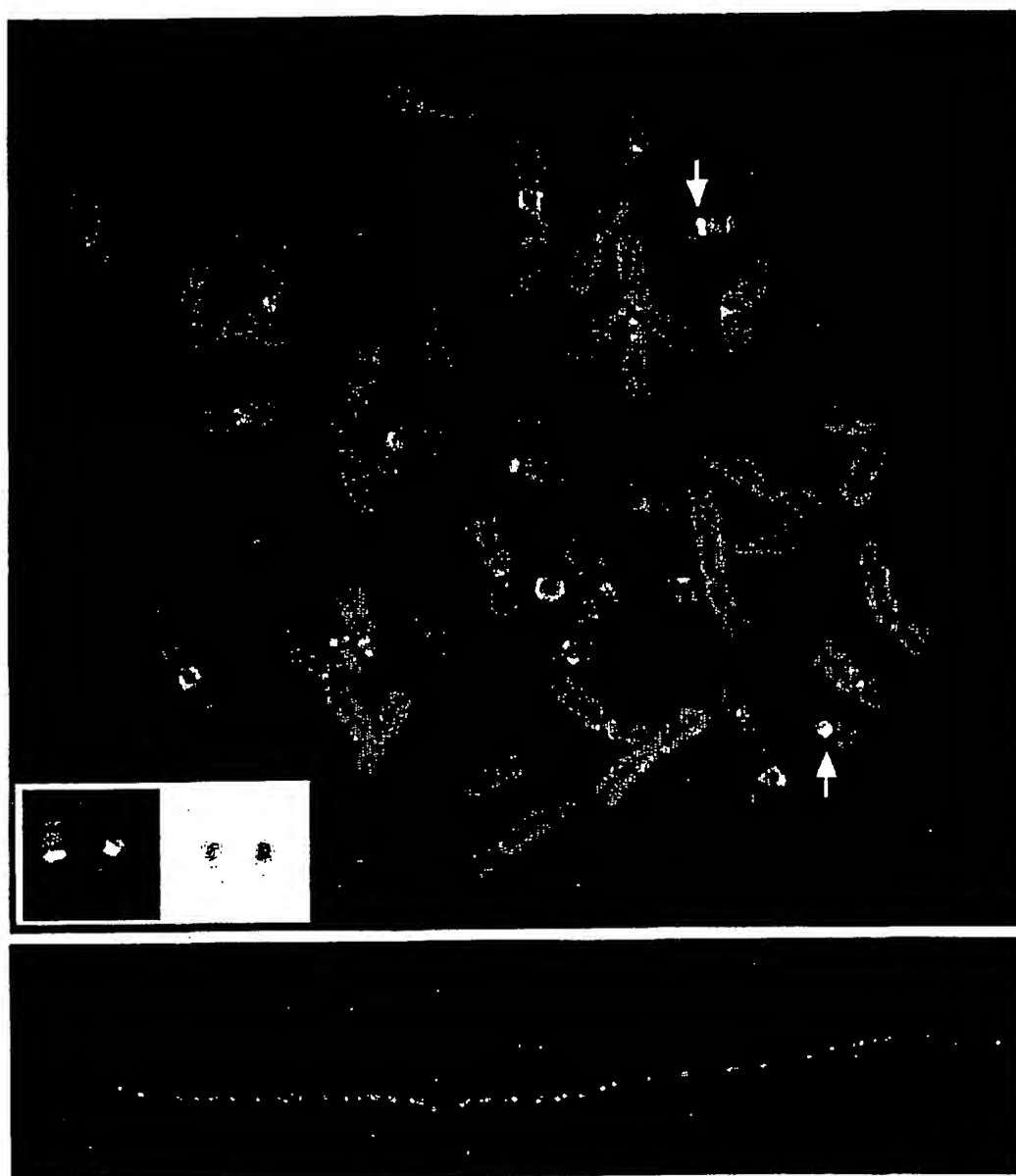


FIG. 21A



FIG. 21B

Spe I digestion of BAC/YACs containing alphoid DNA repeats

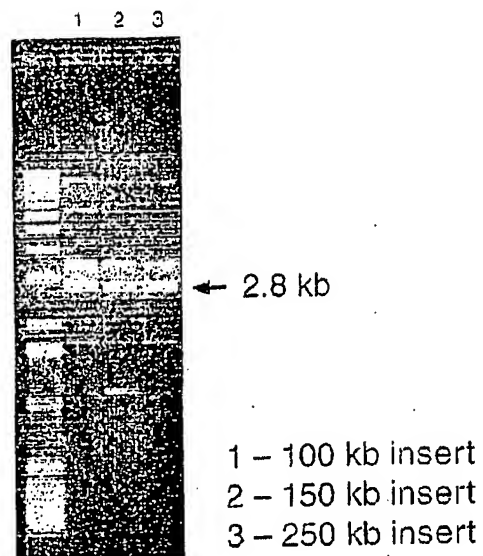


FIG. 22

Alphoid DNA Repeats Contain Yeast Origin of Replication Consensus Sequences

ARS consensus: $\begin{array}{ccccccc} \text{AAAAA} & \text{TTTA} & \text{TA} & & \text{A} & & \\ & \text{TTTT} & \text{CG} & \text{TTT} & \text{T} & \text{GTT} & \end{array}$

tctttgccttgcgtttatcttgcctgctcATTTTTTAATATATTcTTcaaataaatcacattactttata
aaagtagtttctcagaatgcttctgagtAgTTTTTTATGTgAAGATatttccttttccacaataggcct
tgcaatgngngcattcaactcacaagagTtgAAccTATcTTTTGATtgaagattttgaatctttctttt
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FIG. 23

SEQUENCE LISTING

<110> The Government of the United States of America, as represented by the
Secretary, Department of Health and Human Services, c/o Centers for
Disease Control and Prevention

VLADIMIR L. LARIONOV
J. CARL BARRETT
NATALAY KOUPRINA

<120> Artificial Chromosomes That Can Shuttle
Between Bacteria, Yeast and Mammalian Cells

<130> 14014.0385P1

<140> unassigned

<141> 2002-04-08

<150> 60/282,010

<151> 2001-04-06

<160> 54

<170> FastSEQ for Windows Version 4.0

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<211> 1594

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =
Synthetic Construct

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ctctatcaaa	agatcagttc	gtctctgtga	gttgaatgca	tacatcaaaa	agaagcttct	180
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ttttatgtga	agacatttct	tttccctcca	tagtccacaa	agtgtcccaa	atatccactt	600
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gagatgaatg	cacacatcac	aaagaagttt	ctcagaatct	ctctgtgtaa	tttttatgtg	720
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ttttgatgta	tgcatccaac	tcacagagac	gaactgatct	tttgatagag	cagttttgaa	1500
actcactttt	gtagaatctg	caggtggata	tttggagtac	attgcggcct	atggtgaaaa	1560
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<210> 2

<211> 2847

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =
Synthetic Construct

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ctctatcaaa	agatcagttc	gtctctgtga	gttgaatgca	tacatcaaaa	agaagcttct	180
caaaatgctt	ctgtgtgggt	tttcggtgaa	gatagttcct	tttctaccat	aggtctcaaa	240
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tctgggtagt	ttttctgtga	agatagttcc	ttttctacca	tgggccacaa	agggctccaa	420
atacccactt	gcagattcta	caaaaagaga	gtttcacaa	tgctctatca	aacaatatgt	480
tcaactttgt	gggttgaa	caaataatcac	aagaattttc	tccaatgct	tctgtgtagt	540
ttttatgtga	agacatttct	tttccctcca	tagtccacaa	agtgtctcaa	atatccactt	600
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tctaaaaaaa	acagtgtttc	aaaactgctc	aatcaaaaaga	tagttcaact	ctgtgagaag	1860
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gtgggttgaa	tgcacacatc	acaaagaatt	ttctcagaat	gcttctgtgt	agttttcata	2760
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<213> Artificial Sequence

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caaagtgtct	cgaatatcca	cttgagatt	ttactaaaga	gtgtttccaa	actgctcaat	180
caagaggaag	tttcaagtct	gtgagctgaa	cgcacacatc	acaaagtagt	ttctgagaat	240
gcttctgtgt	agtttttatg	tgaagatgtt	ttcttttcca	ccataggctg	caaagggctc	300
caaatatcca	cttgagatt	ctacaaaaag	agagtttcaa	aagtgtctcta	tcaaaagata	360
ggttcaacta	tgtgatatga	atgcacacat	cacaaagtag	tttctcagaa	tgcttctgtg	420
tagtttttat	gtaaagatat	ttccttttcc	accataggcc	tcaaaagcact	ccaaatatcc	480
acttgagat	ctacaaaaaa	gagattttca	aaactattta	atcaaaaagaa	aggttcaaat	540
ctgtcagttg	aaggtacata	tcacaaacaa	gtttatttga	atgcttctgt	gtagttttta	600
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cttttccaca acagcgtgca aaacgcttca aatatgccct tagagattcc acaaaaagag 2880
 tgtttccaaa ctactcaaat caaaaaatga tttcaactct gtgagatgaa tgcacacatc 2940
 acaaactagt 2950

<210> 4
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 <212> DNA
 <213> Artificial Sequence

<220>
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 Synthetic Construct

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 aggcctcaaa gtgctccaaa tattcacttg tacattctac caaacgagta tttcaaaact 60
 gctcaatcaa atggaagggt caaaaccgtg acatgaatgc ccacatcaca aagtagtttc 120
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<210> 5
 <211> 172
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

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 agcgtgcaaa acgcttcaaa tatgccctta gagattccac aaaaagagtg tttccaaact 60
 actcaaatca aaaaatgatt tcaactctgt gagatgaatg cacacatcac aaactagttt 120
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<210> 6
 <211> 170
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

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 ctctatcaaa agatcagttc gtctctgtga gttgaatgca tacatcaaaa agaagcctct 120
 caaaatgctt ctgtgtgggt ttctcgtgaa gatagttctt tttctaccat 170

<210> 7
 <211> 171
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

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 tcaaaatgct tctgggtagt ttttctgtga agatagttcc ttttctacca t 171

<210> 8
 <211> 170
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 8
 gggccacaaa gggctccaaa taccacttg cagattctac aaaaagagag ttccacaact 60
 gctctatcaa acaatatgtt caactttgtg ggttgaacac aaatatcaca agaattttct 120
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<210> 9
 <211> 171
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

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<210> 10
 <211> 170
 <212> DNA
 <213> Artificial Sequence

<220>
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 Synthetic Construct

<400> 10
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 gcacaaaaaa agaaatgttc aattctgttt gatgaatgca cacatcaca aagaatttct 120
 cagaatgctt ctctgtagtt tttatgtgaa gatatttctt ttccacaat 170

<210> 11
 <211> 170
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 11
 aggcctcaaaa gggctccaaa tatccacttc cagattctat gaaaagaata ttccaaaact 60
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 cagaatcctt cagtgtaggt tttatgagaa gataattcct ttccacaat 170

<210> 12
 <211> 170
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

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<310> 13
 <211> 171
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 13
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 actcgatcaa gagatgggtt caactatgtg agttgaatgc acacatcaca aagaactatg 120
 tcggaattct tctgtgtagt ttttatgtga agatatttcc tttccacaa t 171

<210> 14
 <211> 171
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 14
 agacgtcaaa gtgatccaga tatccacttg cagattccac aaaaagagtg tttcaaaagt 60
 gcacaaccaa aagaaagggt caactagggt agatgaatgc acacatcaga aggaagtttc 120
 tcagaatgct tctgcatagc ttttaaggga agatacttcc tttccaaca t 171

<210> 15
 <211> 171
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 15
 aggcctcaaa ccactccaaa tatectcttg gagataccac aaaaagagtg tttgcaaact 60
 gctcaatcaa aagaaagatt taactctgtg agatgaatcc acacatgaca aagaagtttc 120
 tcagaatgct tctgtgtagt ttttatgtga agatatttcc tttccacaa t 171

<210> 16
 <211> 171
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 16
 aagacccaaa aggtccaaa tattcacttg cagattctaa aaaaaacagt gtttcaaac 60
 tgctcaatca aaagatagtt caactctgtg agaagaatgc tcacatcact gagaagtttc 120
 tcagaatgct tctgtgtagt ttttatatga agatatttcc tttcccaccg t 171

<210> 17
 <211> 171
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 17
 aggccacaaa aggtccaaa tatccacttg cagatactat gaaaagagag tttcaaaact 60
 gtcattcaa aagatacgtt caactctgtg gtttgaatgc acacagcaca aagaagtttc 120
 acagaatgtg tctgtgtagt ttttatctgc ggatgtttcc tttccacca t 171

<210> 18
 <211> 168
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 18
 atgcctaaat atttcccaat ttccacttgc agattctaca agaagagtgt ttcaaaactg 60
 ctgtatcaaa taaagttgaa ctctgtgagg tgaatgcaca cagcacaataa tggttttctca 120
 gaatgcttcc ttgttggttt tatatcaaga tgtttccttt tcaacaat 168

<210> 19
 <211> 167
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 19
 aggcctcaaa gtgcttcaaa tgtccacttg cagattctac aaaaagagtg tttcaaaact 60
 gctcaatcaa aagaaagggt cgactctggg aaattaatgc acacatcaca aagaagtttc 120
 tcagcttctg tgtagttttc atgtgaagtt atttcctttt ccacaat 167

<210> 20
 <211> 171
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 20
 aggccgcaaa gggctccaaa tatcaactta cagattctag gaaaagagag tttcaaaact 60
 gctctacgaa aagatagggt gaactctgtg agatgaatgc acacatcaca aagaagtttc 120
 tcagaatgca tctgtgtagt ttttacggga agacatttcc ttttccacca t 171

<210> 21
 <211> 171
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 21
 cttccacaaa ggtctccaag taaccacttg cagattctac agaaagacac tttaaaaact 60
 gctctatcaa aagatcagtt caagtctgtg gtttgaatgc acacatcaca aagaattttc 120
 tcagaatgct tctgtgtagt tttcatatga agatatttcc ttttccacca t 171

<210> 22
 <211> 171
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 22
 aggcctcaaa gcaactccaaa tatccacttg cagattctac aaaaagagat tttcaaaact 60
 agtcaatcaa aagaagggtt caactctgtc agttgaatgc acatcaca aacaagtttc 120
 tcggaatgca tctgtgtagt ttttatgtga agatatttcc ttctccacaa c 171

<210> 23
 <211> 170
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<221> misc_feature
 <222> (0)...(0)
 <223> y = c or t(u)

<400> 23
 aggcctcaaa gtgctccgaa tatccacttg cagattttac taaagagtgt ttccaaactg 60
 ctcaatcaag aggaagtttc aagtctgtga gctgaacgca cacatcaca agtagtttct 120
 gagaatgctt ctgtgtagt tttatgtgaa gatgttcttct ttccaccat 170

<210> 24
 <211> 171
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 24
 aggctgcaaa gggctccaaa tatccacttg cagattctac aaaaagagag tttcaaaagt 60
 gctctatcaa aagatacctt caactatgtg atatgaatgc acacatcaca aagtagtttc 120
 tcacaatgct tctgtgtagt ttttatgtaa agatatttcc ttttccacca t 171

<210> 25
 <211> 171
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 25
 aggctcaaaa gcactccaaa tatccacttg cagattctac aaaaagagat tttcaaaact 60
 atttaatacaa aagaaagggt caaatctgtc agttgaagggt acatatcaca aacaagttta 120
 ttggaatgct tctgtgtagt ttttatgtga agatatttcc ttttccacaa c 171

<210> 26
 <211> 171
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 26
 aggctcaag gtgctccaaa tatccacttg cagatttcac taaaagtgtg tttccaagct 60
 gctcaatcaa gaggaagttt caagtctgtg aggtgaatgc acacattaca aagaagttac 120
 tgagaatgct tctgtgtagt ttttatgtga agatatttcc ttttccaccg c 171

<210> 27
 <211> 170
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 27
 aggctcaaaa ggcgtgcaaa tatccacttg cagattctac aaaaagagag tttcaaaact 60
 gctgtatcaa aagatagggt caactctgcg agttgaataa gcacatcaca aataagtttc 120
 tgggaacgct tctgtatagt tttatgtgaa tatatttcct tttccaccat 170

<210> 28
 <211> 170
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =
Synthetic Construct

<400> 28

atgcctcaaa gcactccaaa tatccacttg cacattatag aaacatagtc tttcaaaaact	60
tgtcaatcaa agaaagggttc aactccgtga gatgagtgc cacatcacag agaagtttct	120
cggaatgttt ctgtgtagtt tttatgtgaa gatattgcct tttccacaat	170

<210> 29

<211> 170

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =
Synthetic Construct

<400> 29

aggcctcaaa gcgttccaaa tatccaattg cagattccac aaaaaaagtt ttttaaaaact	60
gctcaatcaa atgatatagatt aaactctgtg agattagtgc acacatgtca aaaagtttct	120
cagaatgctt ctgtgtactt tttaggggaa gatatttctt tttccaccat	170

<210> 30

<211> 171

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =
Synthetic Construct

<400> 30

cggccacaaa ggactccaaa taaccacatg cagattctag taacacagag tttcaaaaact	60
gctgtatcaa aagataagtt caactctgag agtttagtgc aaccatcgtg aagaagtttc	120
tcagaatgct tctgagtagt gtttatgtga acatatttcc tttccacca t	171

<210> 31

<211> 170

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =
Synthetic Construct

<400> 31

aggcctgaaa gccctccaaa tatccacttg cagatcctac aaaaagaaag tttcgaaatg	60
ctctctcaaa cgatagtttc gactctgtgg tatgaatata cacatcacia agaagtttct	120
cagaatgctt ctgtgtagtt tttaaatgaa gatatttctt tttccaccat	170

<210> 32

<211> 169

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =
Synthetic Construct

<400> 32
aggcctcaaa gcaactccaaa tatgcacttc cagattctac aaaaagagtg tttcagaact 60
gctcaatcaa aaggaagggtt ccagtctgag acaatacac acatcaaaag gtagttttctc 120
agaatgcttc tgtgtagttt ttatgtgaag atattttcct ttccacat 169.

<210> 33
<211> 166
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
Synthetic Construct

<400> 33
aggccacaaa tggctctaaa taccacttta cattttccac aaaaagagag tttcaaaact 60
gctctaccaa aggtaagttt aacgctgtga gttaagaaca tcacaaagaa gttttctcaga 120
atgcttctgt ctagttctta cgtaaagata ttctcttta cacaat 166

<210> 34
<211> 171
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
Synthetic Construct

<400> 34
aggcagaaaa gtgctccaaa tatccacttg aagattctac agaaaccgtg tttcaaaact 60
gccgaatcaa aagaaagggtt caactctgtg agatgaatgc acacataaca aaggagtctc 120
tcagaatgct tctgtgtagc ttttatatga agacatttag tttccacaa c 171

<210> 35
<211> 171
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
Synthetic Construct

<400> 35
aggcctcaaa gctctctcca tatccacttg cagattctac cgaaagagtg cttccaaact 60
gctcaatcaa aagagacatt caaatctgtg aggtgaatgc agacatcgta aagaagtttc 120
tcagaatgct tctgtgtatt tttgtgtga agttattcgt ttttgacca t 171

<210> 36
<211> 166
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
Synthetic Construct

<400> 36
aggcctcaaa gcgttctaaa tatccacttc tagattctac aaaaagagag tttcaaaact 60
actcaacaaa aaggttcaat tctgtgagtt gaaagcaaac atcacaaaga agtttctcag 120
aatgcgtctg ttagtatttg atgtgaagat atttcctttt cacagt 166

<210> 37
 <211> 169
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 37
 agaatgcaaa gggctccaaa tatccacttg gagattctac aaaaagagtt tcaaaaccgc 60
 tctgtcaaat gataggttga actcccgag gtgaatacac acatcacaaa gaggtttctc 120
 agcatgcttc tgtgtagttt ttatgtaaac atatttcggt ttctatcat 169

<210> 38
 <211> 170
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 38
 cctgaaagcc ctccaaatat ccacttgag atctacaaa aagaaagttt cgaaatgctc 60
 tctcaaacga tagtttcgac tctgtggtat gaatacacac atcacaaaga agttttctcag 120
 aatgcttctg tgtagttttt aaatgaagat atttctttt ccaccatagg 170

<210> 39
 <211> 171
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 39
 cctcaaagca ctccaaatat ccacttgag attctacaaa aagagatttt caaaactatt 60
 taatcaaaag aaaggttcaa atctgtcagt tgaaggtaga tatcacaaac aagttttattg 120
 gaatgcttct gtgtagtttt tatgtgaaga tatttccttt tccacaacag g 171

<210> 40
 <211> 171
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 40
 cctcaaagct ctctccatat ccacttgag attctaccga aagagtgcct ccaaactgct 60
 caatcaaaag agacattcaa atctgtgagg tgaatgcaga catcgtaaag aagttttctca 120
 gaatgcttct gtgtattttt tgtgtgaagt tattcgtttt tgcaccatag g 171

<210> 41
 <211> 171
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =
Synthetic Construct

<400> 41

cctcaaagca ctccaaatat ccacttgcag attctacaaa aagagatttt caaaactagt	60
caatcaaaag aaagggttcaa ctctgtcagt tgaatgcaca tatcacaaac aagtttctcg	120
gaatgcgtct gtgtagtttt tatgtgaaga tatttccttc tccacaacag g	171

<210> 42

<211> 171

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =
Synthetic Construct

<400> 42

cctcaaggtg ctccaaatat ccacttgcag atttcactaa aagtgtgttt ccaagctgct	60
caatcaagag gaagtttcaa gtctgtgagg tgaatgcaca cattacaaag aagttactga	120
gaatgcttct gtgtagtttt tatgtgaaga tatttccttt tccaccgcag g	171

<210> 43

<211> 340

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =
Synthetic Construct

<400> 43

cctcaaagcg ctgcaaatat ccacttgcag attctacaaa aagagagttt caaaactgct	60
gtatcaaaag atagggtcaa ctctgcgagt tgaataagca catcacaaat aagtttctgg	120
gaacgcttct gtatagtttt atgtgaatat atttcctttt ccaccatatt cctcaaagca	180
ctccaaatat ccacttgcac attatagaaa catagtcttt caaaacttgt caatcaaga	240
aagggttcaac tccgtgagat gagtgcacac atcacagaga agtttctcgg aatgtttctg	300
tgtagttttt atgtgaagat attgcctttt ccacaatagg	340

<210> 44

<211> 342

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =
Synthetic Construct

<400> 44

cctcaaagcg ttccaaatat ccaattgcag attccacaaa aaaagttttt taaaactgct	60
caatcaaatg atagattaaa ctctgtgaga ttagtgcaca catgtcaaaa aagtttctca	120
gaatgcttct gtgtactttt taggggaaga tatttccttt tccaccatcg gccacaaagg	180
actccaaata accacatgca gattctagta acacagagtt tcaaaactgc tctatcaaaa	240
gataagttca actctgagag tttagtgcac ccatcgtgaa gaagtttctc agaatgttcc	300
tgagtagtgt ttatgtgaag atatttcctt ttccaccata gg	342

<210> 45
 <211> 341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 45
 cctcaaagtg ctccgaatat ccacttgcag attttactaa agagtgtttc caaactgctc 60
 aatcaagagg aagtttcaag tctgtgagct gaacgcacac atcacaaagt agtttctgag 120
 aatgcttctg tgtagttttt atgtgaagat gttttctttt ccaccatagg ctgcaaaggg 180
 ctccaaatat ccacttgcag attctacaaa aagagagttt caaaagtgct ctatcaaaag 240
 ataggttcaa ctatgtgata tgaatgcaca catcacaaag tagtttctca gaatgcttct 300
 gtgtagtttt tatgtaaaga tatttccttt tccaccatag g 341

<210> 46
 <211> 335
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 46
 cctccaagcg ttctaaatat ccacttctag attctacaaa aagagagttt caaaactact 60
 caaacaaaag gttcaattct gtgagttgaa agcaaaccac acaaagaagt ttctcagaat 120
 gcgtctgtgt agttttgatg tgaagatatt tccttttcac agtagaatgc aaagggtctc 180
 aaatatccac ttggagattc tacaaaaaga gtttcaaaac cgctctgtca aatgatagggt 240
 tgaactcccg gaggtgaata cacacatcac aaagaggttt ctgagcatgc ttctgtgtag 300
 tttttatgta aacataattc cgtttctatc atagg 335

<210> 47
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 47
 accgtcgact cacagagttg aa 22

<210> 48
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; Note =
 Synthetic Construct

<400> 48
attcccgttt ccaacgaagg 20

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
Synthetic Construct

<400> 49
gcggatgaat ggcagaaatt cgat 24

<210> 50
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
Synthetic Construct

<400> 50
ccggctcgag ctgtggaatg tgtgtcagtt agg 33

<210> 51
<211> 5250
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
Synthetic Construct

<400> 51
cctgagagca ggaagagcaa gataaaaaggt agtatttgtt ggcgatcccc ctagagtctt 60
ttacatcttc ggaaaacaaa aactattttt tctttaattt ctttttttac tttctatatt 120
taattttatat atttatatta aaaaatttaa attataatta tttttatagc acgtgatgaa 180
aaggacccta agaaaccatt attatcatga cattaacctt taaaaatagg cgtatcacga 240
ggccctttcg tctcgcgcgt ttcggtgatg acggtgaaaa cctctgacac atgcagcacc 300
cggagacggg cacagcttgt ctgtaagcgg atgccgggag cagacaagcc cgtcaggggcg 360
cgtcagcggg tgttggcggg tgtcggggct ggcttaacta tgcggcatca gagcagattg 420
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aaaaaatgag caggcaagat aaacgaaggg aaagatgaca gagcagaaag ccctagtaaa 780
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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/10990

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12N 15/63, 15/85; C07H 21/04

US CL : 435/320.1, 455; 536/23.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/320.1, 455; 536/23.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
WEST, STN, DIALOG, MEDLINE, EMBASE, DERWENT

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	HENNING et al. Human artificial chromosomes generated by modification of a yeast artificial chromosome containing both human alpha satellite and single-copy DNA sequences. Proc. Natl. Acad. Sci. USA. January 1999, Vol. 96, pages 592-597, see especially page 595 and the discussion.	1, 3-5, 8, 17-20, 24-29, 31-34 and 41
X	WO 00/18941 A1 (MEDICAL RESEARCH COUNCIL) 06 April 2000 (06.04.2000) see especially pages 6, 9-11 and the claims.	1-5, 8, 17-21, 24-41
X	FARR et al. Generation of a human X-derived minichromosome using telomere-associated chromosome fragmentation. EMBO Journal. 1995, Vol. 14, No. 21, pages 5444-5454, see especially the figures and the discussion.	1, 3-5, 8, 18, 19, 25-28, 41
—	DE 197 20 839 A1 (SCHINDELHAUER) 19 November 1998 (19.11.1998) see especially column 8.	-----
Y		1-5, 7-12, 18-41
—	US 5,869,294 A (HARRINGTON et al.) 09 February 1999 (09.02.1999) see especially columns 3-6 and the claims	-----
Y		1-5, 7-12, 18-41

☒ Further documents are listed in the continuation of Box C.
 ☐ See patent family annex.

* Special categories of cited documents:	"T"
"A" document defining the general state of the art which is not considered to be of particular relevance	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E" earlier application or patent published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"&c" document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

02 September 2002 (02.09.2002)

Date of mailing of the international search report

19 SEP 2002

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